

CC in the processing of wheat or maize for starch production. (Updated on 17
 CC -OCT-2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 2.7e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFYSYWMDHGVTYTNNGPGGQFVWMSNSGNFVGKMGQPGTKNKVI 60
 DB 1 OTIQPGTGYNNNGYFYSYWMDHGVTYTNNGPGGQFVWMSNSGNFVGKMGQPGTKNKVI 60
 QY 61 NFGSGYNNNGNSYLSYVWGSRNPLIEYIYVENFGTNPSTGATKGEVTSDSGVYDIYRT 120
 DB 61 NFGSGYNNNGNSYLSYVWGSRNPLIEYIYVENFGTNPSTGATKGEVTSDSGVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 2

AA99680
 ID AA99680 standard; protein; 190 AA.

XX
 AC AA99680;

DT 12-SEP-2003 (revised)
 DT 28-SEP-2000 (first entry)

XX
 DE T. reesei xylanase, Xyn II.

XX
 KW Xylanase: animal feed; digestion efficiency; thermostable;
 feed pelleting; enzyme; Xyn A; Xyn B; Xyn; Xyn C; Xyn I; Xyn II.

OS Hypocrea jecorina.

XX
 PN WO200029587-A1.

PD 25-MAY-2000.

PF 16-NOV-1999; 99WO-CA001093.

XX
 PR 16-NOV-1998; 98US-0108504P.

XX
 PA (IOGE-) IOGEN CORP.

PI Sung WL, Tolan JS;

XX
 DR WPI; 2000-387799/33.

XX
 DR N-PSDB; AAA48219.

PT Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.

XX
 PS Disclosure; Fig 1; 86pp; English.

XX
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*
 CC reesei, is a xylanase Family II member. The xylanases of Family II have
 CC several properties suitable for feed applications, however, they lack the
 CC thermostability required to survive food pelleting. The present sequence
 CC was used to identify non-conserved residues in Family II xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.
 CC As a result various thermostable xylanases were identified (AA99683,
 CC AA99684, AA99685, AA99686, AA99735 and AA99736) which would be
 CC useful for animal feeds, especially poultry and swine feed. (Updated on
 CC 12-SEP-2003 to standardise OS field)

XX
 SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 3; Length 190;
 Best Local Similarity 100.0%; Pred. No. 2.7e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFYSYWMDHGVTYTNNGPGGQFVWMSNSGNFVGKMGQPGTKNKVI 60
 DB 1 OTIQPGTGYNNNGYFYSYWMDHGVTYTNNGPGGQFVWMSNSGNFVGKMGQPGTKNKVI 60
 QY 61 NFGSGYNNNGNSYLSYVWGSRNPLIEYIYVENFGTNPSTGATKGEVTSDSGVYDIYRT 120
 DB 61 NFGSGYNNNGNSYLSYVWGSRNPLIEYIYVENFGTNPSTGATKGEVTSDSGVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 3

AAE18452
 ID AAE18452 standard; protein; 190 AA.

XX
 AC AAE18452;

DT 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX
 DE *Trichoderma reesei* xylanase (Trx), Xyn II.

XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; Xyn II.

OS Hypocrea jecorina.

XX
 FH Key Location/Qualifiers

FT Region 151..162
 /note="Helix"

XX
 PN WO200192487-A2.

XX
 PD 06-DEC-2001.

PF 31-MAY-2001; 2001WO-CA000769.

XX
 PR 31-MAY-2000; 2000US-0213803P.

XX
 PA (CANADA) NAT RES COUNCIL CANADA.

PI Sung WL;

XX
 DR WPI; 2002-171435/22.

XX
 DR N-PSDB; AAD29410.

PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.

XX
 PS Disclosure; Page 80-81; 109pp; English.

XX
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and
CC improved digestibility of poultry and swine feed. Modified xylanase has
CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is Trichoderma reesei
CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.7e-89;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQSVNMSNGNPFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQSVNMSNGNPFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSLSYVGWSRNPLIEYIVENFGTNPSTGATKLGCVTSDDSVYDIYRT 120
DB 61 NFSGSYNPNNGNSLSYVGWSRNPLIEYIVENFGTNPSTGATKLGCVTSDDSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4

AAO30259
ID AAO30259 standard; protein; 190 AA.

XX AAO30259;

DT 23-OCT-2003 (revised)
DT 03-SEP-2003 (first entry)

DE Trichoderma reesei xylanase II enzyme (Trx).

KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KW pulp manufacture; poultry feed; swine feed; enzyme.

OS Hypocrea jecorina.

XX WO2003046169-A2.

PD 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

DR WPI: 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from Trichoderma reesei.

XX Claim 1; Fig 2; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 100.0%; Score 1045; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 2.7e-89;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQSVNMSNGNPFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGNNGFYISYVNDGHGVTYTNPGGQSVNMSNGNPFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSLSYVGWSRNPLIEYIVENFGTNPSTGATKLGCVTSDDSVYDIYRT 120
DB 61 NFSGSYNPNNGNSLSYVGWSRNPLIEYIVENFGTNPSTGATKLGCVTSDDSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 5

AAAR47122
ID AAR47122 standard; protein; 223 AA.

XX AAR47122;

DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-JUN-1994 (first entry)

DE PI 9.0 endoxylanase.

KM Trichoderma reesei; enzyme; paper; pulp; food; feed industry; PI 5.5;
KW PI 9.0; xln1; xln2; endoxylanase.

OS Hypocrea jecorina; QM6a.

XX Key Location/Qualifiers

FT Cleavage-site 19..20

FT Protein 34..223

FT Modified-site 71

FT Peptide /label= N-glycosylation_site

FT Modified-site 94 /note= "sequence used for prepn. of PCR primer"

FT Active-site 119 /label= N-glycosylation_site

FT Active-site 210 /note= "Glu proposed to be involved with an active site"

FT Active-site /note= "Glu proposed to be involved with an active site"

XX WO9324621-A1.

XX 09-DEC-1993.

XX 24-MAY-1993; 93WO-FI000221.

XX 29-MAY-1992; 92US-00889893.

XX (ALKO-) ALKO OY AB.

XX Suominen P, Nevalainen H, Saarelainen R, Palohelimo M, Lahtinen T;
PI Fagerstrom R;

DR WPI: 1993-405812/50.
DR N-PSDB; AAO54775.

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed
 PT industry - comprising sequence encoding amino acid sequence of T. reesei
 PT PI 5.5 xylanase.

XX Claim 3; Page 77-78; 11pp; English.

CC The T. reesei xln2 gene coding for the PI 5.0 endoxylanase was isolated
 CC from the wild-type strain QM6. The gene contains one intron of 108
 CC nucleotides and codes for a protein of 223 amino acids in which two
 CC putative N-glycosylation target sites were found. Three different T.
 CC reesei strains were transformed by targeting a construct composed of the
 CC xln2 gene with its own promoter to the endogenous chh1 locus. Highest
 CC overall prodn. levels for xylanase were obtained using the T. reesei
 CC ALKO221, a genetically engineered strain, as a host. Integration into
 CC the chh1 locus was not required for enhanced expression under xln2
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)

SO Sequence 223 AA;

Query Match 100.0%; Score 1045; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 3.3e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QTIGPTGYNNGYFYSYNDGAGVTYNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60
 DB 34 QTIGPTGYNNGYFYSYNDGAGVTYNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93
 OY 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 153
 OY 121 QRVNQPSTIGTATFYQVMSVRNRHSSGSVNTANHFNAHQOGLTLGTMVQIYAVEGYF 180
 DB 154 QRVNQPSTIGTATFYQVMSVRNRHSSGSVNTANHFNAHQOGLTLGTMVQIYAVEGYF 213
 OY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 6
 AAM67567
 ID AAM67567 standard; protein; 223 AA.

XX AAM67567;
 AC
 XX
 DT 17-OCT-2003 (revised)
 DT 02-MAR-1999 (first entry)
 XX
 DE T. reesei xylanase II protein.
 XX
 XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;
 XX degradation; polymer; xylan; carbohydrate; plant; paper; pulp.
 OS Hypocrea jecorina.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "primary signal peptide"
 FT Peptide 20..33
 FT /note= "propeptide"
 FT Protein 33..223
 FT /note= "mature xylanase II protein"
 FT Modified-site 71
 FT /note= "N-glycosylated"
 FT Modified-site 94
 FT /note= "N-glycosylated"
 FT Active-site 119
 FT /note= "active site residue"
 FT Active-site 210
 FT /note= "active site residue"

XX US5837515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1992; 92US-00889893.

XX 24-MAY-1993; 93WO-FI000221.

XX 18-JUN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTIOET OY.

XX Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;
 PI Suominen P;
 XX WPT, 1999-023453/02.
 XX N-PSDB; AAV81332.

PT Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
 PT recombinant production of the enzyme, for use in paper and pulp
 PT production.

PS Claim 3; Fig 3A-B; 52pp; English.

XX This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)
 CC which has an isoelectric point (pI) of 9. The coding sequence was
 CC isolated by reverse transcription PCR using the primers AAV81333-V81335
 CC based on amino acid sequence derived from the N-terminal of the purified
 CC protein. The encoded protein contains a 33 amino acid propeptide sequence
 CC with a primary signal peptide cleavage site between residues 19-20. The
 CC mature protein comprises 190 amino acids with a calculated molecular
 CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer
 CC xylan, one of the most abundant carbohydrate components in plants. This
 CC is especially useful in the paper and pulp making industry. (Updated on
 CC 17-OCT-2003 to standardise OS field)

SO Sequence 223 AA;

Query Match 100.0%; Score 1045; DB 2; Length 223;
 Best Local Similarity 100.0%; Pred. No. 3.3e-89;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QTIGPTGYNNGYFYSYNDGAGVTYNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 60
 DB 34 QTIGPTGYNNGYFYSYNDGAGVTYNGPGGQFSYVMSNSGNFVGKGMQPGTKNKVI 93
 OY 61 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 153
 OY 121 QRVNQPSTIGTATFYQVMSVRNRHSSGSVNTANHFNAHQOGLTLGTMVQIYAVEGYF 180
 DB 154 QRVNQPSTIGTATFYQVMSVRNRHSSGSVNTANHFNAHQOGLTLGTMVQIYAVEGYF 213
 OY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 7
 AAE18470
 ID AAE18470 standard; protein; 190 AA.

XX AAE18470;
 AC
 XX
 DT 16-MAY-2002 (first entry)
 DT Trichoderma reesei xylanase mutant, Trx-75A.
 XX
 XX Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.


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XX Hypocrea jecorina.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 75
FT /note= "Wild type Ser substituted with Ala"
XX WO200192487-A2.
XX
XX 06-DEC-2001.
XX
XX 31-MAY-2001; 2001WO-CA000769.
XX
XX 31-MAY-2000; 2000US-0213803P.
XX
XX (CANADA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2002-171435/22.
XX
XX Modified xylanase exhibiting increased thermostability and
XX PT alkalophilicity useful for industrial processing e.g. for pulp
XX PT manufacturing.
XX
XX Claim 42; Page; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX CC thermostability and alkalophilicity. Modified xylanase is useful in
XX CC industrial process such as pulp manufacturing. Modified xylanase is also
XX CC useful for bleaching of pulp, processing of precision devices and
XX CC improving digestibility of poultry and swine feed. Modified xylanase has
XX CC improved performance at conditions of high temperature and pH and
XX CC exhibits improved thermostability and/or alkalophilicity in comparison to
XX CC corresponding native xylanase. The present sequence is Trichoderma reesei
XX CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX CC specification but is derived from wild type xylanase referred as SEQ ID
XX CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX
XX Sequence 190 AA:
SQ
Query Match 99.7%; Score 1042; DB 5; Length 190;
Best Local Similarity 99.5%; Pred. No. 5,1e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 OTIQPGTGYNNNGYFYYSYNNNDHGQVYTYNPGGQGFVYVMSNSGNFVGGKGMQPGTKNKVI 60
DB 1 OTIQPGTGYNNNGYFYYSYNNNDHGQVYTYNPGGQGFVYVMSNSGNFVGGKGMQPGTKNKVI 60
QY 61 NFGSGYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKLGCVTSDSGVYDIYRT 120
DB 61 NFGSGYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKLGCVTSDSGVYDIYRT 120
QY 121 QRYNPSIIGTATFYQVMSVRRNHSQSVNTAHNFNAACQGLTGTMDYQIVAVEGYF 180
DB 121 QRYNPSIIGTATFYQVMSVRRNHSQSVNTAHNFNAACQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

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XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutain.
XX
XX Hypocrea jecorina.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 75
FT /note= "Wild type Ser substituted with Ala"
XX WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002WO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANADA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
XX PT thermostability, alkalophilicity and expression efficiency, in comparison
XX PT to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX CC thermostability, alkalophilicity and expression efficiency, in comparison
XX CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX CC is useful for the bleaching of pulp, processing of precision devices and
XX CC for improving digestibility of poultry and swine feed. The present
XX CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX CC sequence is not shown in the specification but is derived from
XX CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX CC in figure 2 of the specification (AA030259)
XX
XX Sequence 190 AA:
SQ
Query Match 99.7%; Score 1042; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 5,1e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 OTIQPGTGYNNNGYFYYSYNNNDHGQVYTYNPGGQGFVYVMSNSGNFVGGKGMQPGTKNKVI 60
DB 1 OTIQPGTGYNNNGYFYYSYNNNDHGQVYTYNPGGQGFVYVMSNSGNFVGGKGMQPGTKNKVI 60
QY 61 NFGSGYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKLGCVTSDSGVYDIYRT 120
DB 61 NFGSGYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKLGCVTSDSGVYDIYRT 120
QY 121 QRYNPSIIGTATFYQVMSVRRNHSQSVNTAHNFNAACQGLTGTMDYQIVAVEGYF 180
DB 121 QRYNPSIIGTATFYQVMSVRRNHSQSVNTAHNFNAACQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

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XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mucin.
XX Hypocrea jecorina.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 161 /note= "Wild type Gln substituted with Arg"
XX FT
XX WO2003046169-A2.
XX PN
XX 05-JUN-2003.
XX PD
XX 20-NOV-2002; 2002MO-CA001758.
XX PF
XX 21-NOV-2001; 2001US-00990874.
XX PR
XX (CANADA) NAT RES COUNCIL CANADA.
XX PA
XX Sung WL;
XX PI
XX WPI; 2003-513647/48.
XX DR
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX PS Example 1; Page; 105pp; English.
XX CC The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AA030259)
XX CC
XX SQ Sequence 190 AA;
Query Match 99.6%; Score 1041; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 6.3e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 OTIOGTGNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKGMQPGTKKVI 60
DB 1 OTIOGTGNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKGMQPGTKKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 GRVNOPSTIIGTATFEYQVSVRRNHRSSGSVNTANHFNMAOGLTLGTMQCIYAVEGYF 180
DB 121 GRVNOPSTIIGTATFEYQVSVRRNHRSSGSVNTANHFNMAOGLTLGTMQCIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190
RESULT 10
AA030301
ID AA030301 standard; protein; 190 AA.
XX AC
XX AA030301;
XX AC
XX 03-SEP-2003 (first entry)
XX DT
XX

DE Trichoderma reesei xylanase II mutant protein (S75G).
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mucin.
XX Hypocrea jecorina.
XX Synthetic.
XX Key Location/Qualifiers
XX Misc-difference 75 /note= "Wild type Ser substituted with Gly"
XX FT
XX WO2003046169-A2.
XX PN
XX 05-JUN-2003.
XX PD
XX 20-NOV-2002; 2002MO-CA001758.
XX PF
XX 21-NOV-2001; 2001US-00990874.
XX PR
XX (CANADA) NAT RES COUNCIL CANADA.
XX PA
XX Sung WL;
XX PI
XX WPI; 2003-513647/48.
XX DR
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX PS Example 1; Page; 105pp; English.
XX CC The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AA030259)
XX CC
XX SQ Sequence 190 AA;
Query Match 99.6%; Score 1041; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 6.3e-89;
Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 OTIOGTGNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKGMQPGTKKVI 60
DB 1 OTIOGTGNNGYFYSYNNDGSGVYTNNGPGQGFVYVMSNSGNFVGGKGMQPGTKKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 GRVNOPSTIIGTATFEYQVSVRRNHRSSGSVNTANHFNMAOGLTLGTMQCIYAVEGYF 180
DB 121 GRVNOPSTIIGTATFEYQVSVRRNHRSSGSVNTANHFNMAOGLTLGTMQCIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190
RESULT 11
AAB48541
ID AAB48541 standard; protein; 190 AA.
XX AC
XX AAB48541;
XX AC
XX 12-SEP-2003 (revised)
XX DT
XX

05-MAR-2001 (first entry)
 XX Trichoderma reesei xyn II xylanase.
 XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
 KW bleaching agent.
 XX Hypocrea jecorina.
 OS WO200068396-A2.
 XX PN
 XX 16-NOV-2000.
 PD 12-MAY-2000; 2000WO-US013172.
 PF 12-MAY-1999; 99US-0133714P.
 PR 12-MAY-1999; 99US-0133714P.
 XX (XENC-) XENCOR INC.
 PA Bentzien JM;
 XX WPI; 2000-678800/66.
 DR
 XX Non naturally occurring XA protein with enhanced thermostability,
 PT alkalophilicity or thermostability relative to the naturally occurring
 PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
 PS Disclosure; Fig 16J; 114pp; English.
 XX The present sequence is given in a specification relating to non
 CC naturally occurring xylanase activity (XA) proteins. The XA proteins
 CC comprise an amino acid sequence less than 97% identical to a naturally
 CC occurring Bacillus circulans xylanase. They are modified to exhibit
 CC enhanced thermostability, alkalophilicity or thermostability relative to
 CC the naturally occurring B. circulans xylanase. They may be used as the
 CC active compound in a bleaching agent which is used for bleaching pulp.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 XX Sequence 190 AA;
 SQ
 Query Match 99.5%; Score 1040; DB 3; Length 190;
 Best Local Similarity 100.0%; Pred. No. 7.8e-89;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TIQPGTGNNGYFYSYVNDHGCVTYTNGPGQFVSVMNSGNFVGKGMQPGTKNKVYN 61
 Db 2 TIQPGTGNNGYFYSYVNDHGCVTYTNGPGQFVSVMNSGNFVGKGMQPGTKNKVYN 61
 QY 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTO 121
 Db 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTO 121
 QY 122 RVNQPSTIIIGTATFYQYVSVRRNHRSSGSVNTANHFMAAQGLTLGTMVQIVAVEGYFS 181
 Db 122 RVNQPSTIIIGTATFYQYVSVRRNHRSSGSVNTANHFMAAQGLTLGTMVQIVAVEGYFS 181
 QY 182 SGSASITVS 190
 Db 182 SGSASITVS 190

RESULT 12
 ID AAO18647 standard; protein; 190 AA.
 AC AAO18647;
 XX 29-AUG-2003 (revised)
 DT 24-OCT-2002 (first entry)
 XX T reesei xyn II xylanase.
 DE
 XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

liquid clarification; coffee extraction; plant oil extraction;
 KW starch extraction; food thickener; animal food additive; mutant; mutein.
 XX Hypocrea jecorina.
 OS WO200238746-A2.
 XX PN
 XX 16-MAY-2002.
 PD 09-NOV-2001; 2001WO-US048018.
 PF 10-NOV-2000; 2000US-00710050.
 PR (XENC-) XENCOR INC.
 PA Bentzien J, Dahiyat B;
 XX WPI; 2002-608200/65.
 DR
 XX Novel xylanase activity protein, useful in bleaching process of pulp and
 PT in food and animal feed industry, has enhanced thermostability and
 PT alkalophilicity.
 PS Disclosure; Fig 16J; 121pp; English.
 XX The present invention relates to a non-naturally occurring xylanase
 CC activity (XA) protein comprising an amino acid sequence less than 97%
 CC identical to a naturally occurring Bacillus circulans xylanase, where the
 CC protein has been modified to exhibit enhanced thermostability,
 CC alkalophilicity, or thermostability relative to naturally occurring B.
 CC circulans xylanase, and has at least 5 amino acid substitutions. A
 CC bleaching agent comprising a modified xylanase is useful for bleaching
 CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
 CC clarifying juice and wine, extracting coffee, plant oils and starch,
 CC improving food thickeners, altering texture in bakery products, e.g.
 CC wheat and corn for starch production, use as animal food additives to aid
 CC in the digestibility of feedstuffs and in the washing of super precision
 CC devices and semiconductors. The present sequence is a xylanase protein
 CC described in the exemplification of the invention. (Updated on 29-AUG-
 CC 2003 to standardise OS field)
 XX Sequence 190 AA;
 SQ
 Query Match 99.5%; Score 1040; DB 5; Length 190;
 Best Local Similarity 100.0%; Pred. No. 7.8e-89;
 Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TIQPGTGNNGYFYSYVNDHGCVTYTNGPGQFVSVMNSGNFVGKGMQPGTKNKVYN 61
 Db 2 TIQPGTGNNGYFYSYVNDHGCVTYTNGPGQFVSVMNSGNFVGKGMQPGTKNKVYN 61
 QY 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTO 121
 Db 62 FSGSYNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKLGVTSDGSVYDIYRTO 121
 QY 122 RVNQPSTIIIGTATFYQYVSVRRNHRSSGSVNTANHFMAAQGLTLGTMVQIVAVEGYFS 181
 Db 122 RVNQPSTIIIGTATFYQYVSVRRNHRSSGSVNTANHFMAAQGLTLGTMVQIVAVEGYFS 181
 QY 182 SGSASITVS 190
 Db 182 SGSASITVS 190

RESULT 13
 ID AAO30304 standard; protein; 190 AA.
 AC AAO30304;
 XX 03-SEP-2003 (first entry)
 DT

DE Trichoderma reesei xylanase II mutant protein (N11D).
XX
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutain.
XX
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH MISC-difference 11 /note= "Wild type Asn substituted with Asp"
FT
XX
XX WO2003046169-A2.
PN
XX 05-JUN-2003.
PD
XX 20-NOV-2002; 2002WO-CA001758.
PF
XX 21-NOV-2001; 2001US-00990874.
PR
XX (CANA) NAT RES COUNCIL CANADA.
PA
XX Sung WL;
PI
XX WPI; 2003-513647/48.
DR
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
PS
XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AA030259)
XX
XX Sequence 190 AA;
SQ
Query Match 99.5%; Score 1040; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 7.8e-89;
Matches 189; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQGTGNNNGYFYSYNNNDGHSVTTNPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
DB 1 OTIQGTGNNNGYFYSYNNNDGHSVTTNPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
QY 61 NFSGSYNPENGNSYLSVYSGMSRNPYLEYIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPENGNSYLSVYSGMSRNPYLEYIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAAOQGLTGMDYQIYAVEGYF 180
DB 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAAOQGLTGMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
AA030299
ID AA030299 standard; protein; 190 AA.
XX
AC AA030299;
XX
DT 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (L105R).
DE
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutain.
XX
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH MISC-difference 105 /note= "Wild type Leu substituted with Arg"
FT
XX
XX WO2003046169-A2.
PN
XX 05-JUN-2003.
PD
XX 20-NOV-2002; 2002WO-CA001758.
PF
XX 21-NOV-2001; 2001US-00990874.
PR
XX (CANA) NAT RES COUNCIL CANADA.
PA
XX Sung WL;
PI
XX WPI; 2003-513647/48.
DR
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
PS
XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AA030259)
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XX Sequence 190 AA;
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Query Match 99.4%; Score 1039; DB 7; Length 190;
Best Local Similarity 99.5%; Pred. No. 9.6e-89;
Matches 189; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTIQGTGNNNGYFYSYNNNDGHSVTTNPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
DB 1 OTIQGTGNNNGYFYSYNNNDGHSVTTNPGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
QY 61 NFSGSYNPENGNSYLSVYSGMSRNPYLEYIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPENGNSYLSVYSGMSRNPYLEYIVENFGTYPNSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAAOQGLTGMDYQIYAVEGYF 180
DB 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNAAOQGLTGMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
AAW60284
ID AAW60284 standard; protein; 190 AA.
XX
AC AAW60284;
XX

02-SEP-1998 (first entry)

Modified xylanase II of Trichoderma reesei.

Family 11 xylanase; improve; thermophilicity; alkalophilicity;
thermotolerance; bleach; wood pulp; processing; wheat; maize;
digestibility-improving animal feed additive; starch production; mutant.

Synthetic.

Hypocrea jecorina.

Key Location/Qualifiers

Misc-difference 14

/label= F14X

/note= "this residue can be Tyr or Phe"

EP828002-A2.

11-MAR-1998.

05-SEP-1997; 97EP-00115412.

09-SEP-1996; 96US-00709912.

(CANA) NAT RES COUNCIL CANADA.

Sung WL, Yaguchi M, Ishikawa K;

WPI; 1998-161100/15.

Modified xylanase enzymes - useful for improving wood pulp bleaching,
etc.

Claim 5; Page; 84pp; English.

The present sequence represents a modified xylanase of Trichoderma
reesei. The specification describes a method for modifying a Family 11
xylanase to improve its thermophilicity, alkalophilicity and or
thermotolerance. This method comprises modification of amino acids 10,
14, 27 or 29 of Trichoderma reesei xylanase II or the corresponding
aligned amino acids of another Family 11 xylanase, replacement of one or
more amino acid sequences in the N-terminal region with corresponding
aligned sequences from another family 11 xylanase to form a chimeric
xylanase and/or upstream extension of the N terminus by addition of upto
10 amino acids. The modified xylanases are useful for improving the
bleachability of wood pulp by treatment at 55-75 degrees celsius and pH
7.5-9.0 for 5-180 minutes. They might also be useful as digestibility-
improving animal feed additives. They might also be useful in the
processing of wheat or maize for starch production. note: this sequence
does not appear in the specification; it was created using information
provided

Sequence 190 AA;

Query Match 99.3%; Score 1038; DB 2; Length 190;
Best Local Similarity 99.5%; Pred. No. 1.2e-88;

Matches 189; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYMNDGAGVTYNGPGQFSYVMSNSGNFVGKGMQPGTKNKYI 60
Db 1 QTIQPGTGNNGYXYSYWNDDGAGVTYNGPGQFSYVMSNSGNFVGKGMQPGTKNKYI 60

QY 61 NFGSYVNPNGNSYLSYVGWRNPLIEYIYVENFGTYNPSGTATKLGAVTSDGSVDIYRT 120
Db 61 NFGSYVNPNGNSYLSYVGWRNPLIEYIYVENFGTYNPSGTATKLGAVTSDGSVDIYRT 120

QY 121 QRVNPSIIIGTATFYQYWSVRNHRSSGSVNTANHFNAQAQGLITGMDYQIVAVEGYF 180
Db 121 QRVNPSIIIGTATFYQYWSVRNHRSSGSVNTANHFNAQAQGLITGMDYQIVAVEGYF 180

QY 181 SSGSASTIVS 190
Db 181 SSGSASTIVS 190

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Job time : 48.5 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)
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Title: US-09-856-025B-16

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	190	US-10-307-441-16	Sequence 16, Appl
2	1045	100.0	222	US-10-237-386-32	Sequence 32, Appl
3	1045	100.0	223	US-10-237-386-31	Sequence 31, Appl
4	1035	99.0	190	US-10-307-441-17	Sequence 17, Appl
5	1033	98.9	223	US-10-237-386-30	Sequence 30, Appl
6	996	95.3	190	US-10-307-441-14	Sequence 14, Appl
7	990	94.7	190	US-10-237-386-33	Sequence 33, Appl
8	876	83.8	223	US-10-237-386-34	Sequence 34, Appl
9	765.5	73.3	241	US-10-237-386-35	Sequence 35, Appl
10	705.5	67.5	219	US-10-237-386-29	Sequence 29, Appl
11	685	65.6	313	US-10-213-990-72	Sequence 72, Appl
12	680.5	65.1	227	US-10-237-386-22	Sequence 22, Appl
13	678.5	64.9	227	US-10-237-386-21	Sequence 21, Appl
14	675.5	64.6	234	US-10-213-990-69	Sequence 69, Appl
15	671.5	64.3	189	US-10-307-441-19	Sequence 19, Appl

16	669.5	64.1	221	US-10-213-990-66	Sequence 66, Appl
17	664.5	63.6	225	US-10-237-386-36	Sequence 36, Appl
18	656	62.8	221	US-10-237-386-37	Sequence 37, Appl
19	650.5	62.2	221	US-10-237-386-20	Sequence 20, Appl
20	647.5	62.0	223	US-10-299-393-2	Sequence 2, Appl
21	647	61.9	217	US-09-790-070A-11	Sequence 11, Appl
22	635.5	60.8	194	US-10-307-441-20	Sequence 20, Appl
23	635.5	60.8	225	US-09-467-368-2	Sequence 2, Appl
24	635.5	60.8	225	US-10-237-386-24	Sequence 24, Appl
25	635.5	60.8	231	US-10-237-386-26	Sequence 26, Appl
26	629.5	60.2	221	US-10-237-386-44	Sequence 44, Appl
27	628.5	60.1	221	US-10-237-386-25	Sequence 25, Appl
28	614.5	58.8	227	US-10-237-386-27	Sequence 27, Appl
29	609.5	58.3	239	US-10-237-386-40	Sequence 40, Appl
30	608.5	58.2	241	US-10-237-386-43	Sequence 43, Appl
31	607.5	58.1	189	US-10-307-441-13	Sequence 13, Appl
32	607.5	58.1	240	US-10-237-386-42	Sequence 42, Appl
33	598	57.2	228	US-10-237-386-39	Sequence 39, Appl
34	596	57.0	216	US-10-237-386-45	Sequence 45, Appl
35	595.5	57.0	344	US-09-770-621-2	Sequence 2, Appl
36	595.5	57.0	344	US-10-286-993-2	Sequence 2, Appl
37	591.5	56.6	242	US-10-237-386-41	Sequence 41, Appl
38	589	56.4	191	US-10-307-441-10	Sequence 10, Appl
39	571.5	54.7	233	US-10-237-386-28	Sequence 28, Appl
40	565.5	54.1	197	US-10-307-441-9	Sequence 9, Appl
41	565.5	54.1	201	US-10-237-386-43	Sequence 23, Appl
42	536.5	51.3	237	US-10-237-386-47	Sequence 47, Appl
43	528.5	50.6	226	US-10-237-386-63	Sequence 63, Appl
44	527.5	50.5	189	US-10-307-441-12	Sequence 12, Appl
45	526.5	50.4	236	US-10-237-386-46	Sequence 46, Appl

ALIGNMENTS

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RESULT 1
US-10-307-441-16
; Sequence 16, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-307-441-16

Query Match      100.0%  Score 1045; DB 14; Length 190;
Best Local Similarity 100.0%  Pred. No. 1.9e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QTIQPGTGYNNGYFYSYWMDHGVTYNNPGQGFVSVMNSGNGFVGKQWPGTKNRYI 60
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QY      121 QEVNPSIIIGATFYQYWSVRNRRSSGSVNTAHFNMAQOGLTLGMDYQIVAVEGYF 180
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Db 121 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 2
US-10-237-386-32

; Sequence 32, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-32

Query Match 100.0%; Score 1045; DB 14; Length 222;
Best Local Similarity 100.0%; Pred. No. 2,4e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 93 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 152
QY 121 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180
Db 153 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 212
QY 181 SSGSASITVS 190
Db 213 SSGSASITVS 222

RESULT 3

US-10-237-386-31
; Sequence 31, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-31

Query Match 100.0%; Score 1045; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2,4e-94;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYVNDGSGVTTNGGQGFVYVNSGNGFVGKGMQPGTKXKI 60
Db 34 OTIQPGTGYNNGYFYSYVNDGSGVTTNGGQGFVYVNSGNGFVGKGMQPGTKXKI 93
QY 61 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 94 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 153
QY 121 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180
Db 154 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 4

US-10-307-441-17
; Sequence 17, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma viride
US-10-307-441-17

Query Match 99.0%; Score 1035; DB 14; Length 190;
Best Local Similarity 98.9%; Pred. No. 1,9e-93;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNGYFYSYVNDGSGVTTNGGQGFVYVNSGNGFVGKGMQPGTKXKI 60
Db 1 OTIQPGTGYNNGYFYSYVNDGSGVTTNGGQGFVYVNSGNGFVGKGMQPGTKXKI 60
QY 61 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 61 NFSGSYNPNNGSYLSVYVMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180
Db 121 QRVNPSIIIGTATFYQVSVRRNRSSGSVNTANHFNAQAQGLTLGTMVQIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 5
US-10-237-386-30

/ Sequence 30, Application US/10237386
/ Publication No. US20030180895A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Sorensen, Ole
/ APPLICANT: Sorensen, Jens
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
/ FILE REFERENCE: 674509-2046
/ CURRENT APPLICATION NUMBER: US/10/237,386
/ PRIOR FILING DATE: 2002-12-06
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: GB 0005585.5
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: GB 0015751.1
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 30
/ LENGTH: 223
/ TYPE: PRT
/ ORGANISM: T. reesei
US-10-237-386-30

Query Match 98.9%; Score 1033; DB 14; Length 223;
Best Local Similarity 98.9%; Pred. No. 3.6e-93;

Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60
DB 34 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 93
QY 61 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
DB 94 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 153
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 180
DB 154 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 6

US-10-307-441-14
/ Sequence 14, Application US/10307441
/ Publication No. US2003016236A1
/ GENERAL INFORMATION:
/ APPLICANT: Sung, Wing L.
/ APPLICANT: National Research Council of Canada
/ TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
/ FILE REFERENCE: 027367-5006US
/ CURRENT APPLICATION NUMBER: US/10/307,441
/ PRIOR FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: PCT/CA01/00769
/ PRIOR FILING DATE: 2001-05-31
/ PRIOR APPLICATION NUMBER: 60/213,803
/ PRIOR FILING DATE: 2000-05-31
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 190
/ TYPE: PRT
/ ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match 95.3%; Score 966; DB 14; Length 190;
Best Local Similarity 94.7%; Pred. No. 1.2e-89;

Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60
DB 1 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7

US-10-237-386-33
/ Sequence 33, Application US/10237386
/ Publication No. US20030180895A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Sorensen, Ole
/ APPLICANT: Sorensen, Jens
/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
/ FILE REFERENCE: 674509-2046
/ CURRENT APPLICATION NUMBER: US/10/237,386
/ PRIOR FILING DATE: 2002-12-06
/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: GB 0005585.5
/ PRIOR FILING DATE: 2000-03-08
/ PRIOR APPLICATION NUMBER: GB 0015751.1
/ PRIOR FILING DATE: 2000-06-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 33
/ LENGTH: 190
/ TYPE: PRT
/ ORGANISM: T. harzianum
US-10-237-386-33

Query Match 94.7%; Score 990; DB 14; Length 190;
Best Local Similarity 94.2%; Pred. No. 4.8e-89;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60
DB 1 QTIQPGTYNNNGYFYSYVNDGAGVYTNNGPGGQFVSVMNSGNGFVGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMSSNPPLIEYIVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFMAAQQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8

US-10-237-386-34
/ Sequence 34, Application US/10237386
/ Publication No. US20030180895A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
/ APPLICANT: Sorensen, Ole

APPLICANT: Sorensen, Jens
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/10/237,386
 CURRENT FILING DATE: 2002-12-06
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 34
 LENGTH: 223
 TYPE: PRT
 ORGANISM: T. vitride
 US-10-237-386-34

Query Match 83.8%; Score 876; DB 14; Length 223;
 Best Local Similarity 82.1%; Pred. No. 9e-78;
 Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 CTGPGTGYNGCYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKI 60
 DB 34 CTGPGTGYNGCYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKI 93
 QY 61 NFGSYNPGNSYLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRT 120
 DB 94 NFGSYNPGNSYLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRT 153
 QY 121 ORNOPSTIGTATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCF 180
 DB 154 ORNOPSTIGTATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGNANINVS 223

RESULT 9

US-10-237-386-35
 Sequence 35, Application US/10237386
 Publication No. US20030180895A1
 GENERAL INFORMATION:
 APPLICANT: Danisco A/S
 APPLICANT: Sorensen, Ole
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/10/237,386
 CURRENT FILING DATE: 2002-12-06
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 35
 LENGTH: 241
 TYPE: PRT
 ORGANISM: C. gracile
 US-10-237-386-35

Query Match 73.3%; Score 765.5; DB 14; Length 241;
 Best Local Similarity 73.8%; Pred. No. 6.9e-67;
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKIYNSGSY 66
 DB 38 TGYNNGYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKIYNSGSY 96

QY 67 NFGNSYLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRTORVNO 126
 DB 97 NFGNSYLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRTORVNO 156
 QY 127 STIGATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCFSSGSAS 186
 DB 157 STIGATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCFSSGSAS 216
 QY 187 ITV 189
 DB 217 VNV 219

RESULT 10

US-10-237-386-29
 Sequence 29, Application US/10237386
 Publication No. US20030180895A1
 GENERAL INFORMATION:
 APPLICANT: Danisco A/S
 APPLICANT: Sorensen, Ole
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/10/237,386
 CURRENT FILING DATE: 2002-12-06
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 29
 LENGTH: 219
 TYPE: PRT
 ORGANISM: C. gracile
 US-10-237-386-29

Query Match 67.5%; Score 705.5; DB 14; Length 219;
 Best Local Similarity 68.1%; Pred. No. 4.7e-61;
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGYNNGYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKIYNSGS 65
 DB 36 GTGYNNGYFYSYWMDHGGVYTYNGPGGCPFSVWMSNGMFVGGKMGQPGTKXKIYNSGS 94
 QY 66 YNPNNGSTLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRTORVNO 125
 DB 95 YNPNNGSTLSVYGMSRNPLEYIVENFGTYNDSGTATLGEVTSDDGYDIYRTORVNO 154
 QY 126 PSLIGTATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCFSSGSAS 185
 DB 155 PSLIGTATFYQYNSVRNHRSSGSVNTANHFMAAQGLTGMDOYQIVAYGCFSSGSAS 214
 QY 186 SITVS 190
 DB 215 SITVS 219

RESULT 11

US-10-213-990-72
 Sequence 72, Application US/10213990
 Publication No. US20030082595A1
 GENERAL INFORMATION:
 APPLICANT: Danisco A/S
 APPLICANT: Sorensen, Ole
 TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUJIGATUS ENCODING INDUSTRIAL
 FILE REFERENCE: 10182-019-999

;; CURRENT APPLICATION NUMBER: US/10/213,990
;; CURRENT FILING DATE: 2002-08-05
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 72
;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Aspergillus
US-10-213-990-72

Query Match 65.6%; Score 685; DB 14; Length 313;
Best Local Similarity 64.2%; Pred. No. 7.5e-59;
Matches 124; Conservative 29; Mismatches 36; Indels 4; Gaps 3;

QY 1 QTIQPG-TCYNNNGFYSYNNDGAGVYTNPGGQGFYSVMS--NSGNFVGSKGMPGTKN 57
DB 32 QTIITSGCTGNNGYISWTNAGSVQYTNAGGERISVTMANONGDFTCKGMNPSGDH 91
QY 58 KVINFGSYNPNNGSYLSVYGSNRPILLEYIVENFGTNPSTGATKLGVTSDGSYYDI 117
DB 92 D-IIFSGSFPNSGNAYLSVYGMTNPLVEYYILEYVGSYNPGSGWTHKGVTSDGSTYDI 150
QY 118 YRTGRVNPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 177
DB 151 YEHQOVNPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 210
QY 178 GYFSSGSASITVS 190
DB 211 GYBSGCTSTIVS 223

RESULT 12
US-10-237-386-22
; Sequence 22, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 227
; TYPE: PRT
; ORGANISM: A. pisi
US-10-237-386-22

Query Match 65.1%; Score 680.5; DB 14; Length 227;
Best Local Similarity 65.3%; Pred. No. 1.4e-58;
Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;

QY 2 TIQPGT-----GYNNGFYSYNNDGAGVYTNPGGQGFYSVMS--NSGNFVGSKGMPGTKN 57
DB 34 TARGTSSSGCTHNGCYISWTNAGSVQYTNAGGERISVTMANONGDFTCKGMNPSGDH 92
QY 58 KVINFGSYNPNNGSYLSVYGSNRPILLEYIVENFGTNPSTGATKLGVTSDGSYYDI 117
DB 93 RTIYSGTSPSGNSYLAIVGMTNPLVEYYILEYVGSYNPGSGWTHKGVTSDGSTYDI 152
QY 118 YRTGRVNPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 177
DB 153 AQTGRVNPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 212

QY 178 GYFSSGSASITVS 190
DB 213 GYBSGCTSTIVS 225

RESULT 13
US-10-237-386-21
; Sequence 21, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 227
; TYPE: PRT
; ORGANISM: H. turcicum
US-10-237-386-21

Query Match 64.9%; Score 678.5; DB 14; Length 227;
Best Local Similarity 64.7%; Pred. No. 2.2e-58;
Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;

QY 1 QTIQPGTGNNGFYSYNNDGAGVYTNPGGQGFYSVMS--NSGNFVGSKGMPGTKN 60
DB 37 QSTPNSEGTNNGCYISWTNAGSVQYTNAGGERISVTMANONGDFTCKGMNPSGDH 95
QY 61 NFGSGYNPNNGSYLSVYGSNRPILLEYIVENFGTNPSTGATKLGVTSDGSYYDI 120
DB 96 TISGCTNPNNGSYLAIVGMTNPLVEYYILEYVGSYNPGSGWTHKGVTSDGSTYDI 155
QY 121 QRVNPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 180
DB 156 TRNCPSTIGATFYQVMSVRNRHSSGSVNTAHFNMAAQGLTGMQIYAVE 215
QY 181 SSGSASITVS 190
DB 216 SSGSASITVS 225

RESULT 14
US-10-213-990-69
; Sequence 69, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUWIGATUS ENCODING INDUSTRIAL
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-69

Query Match	64.6%;	Score 675.5;	DB 14;	Length 234;
Best Local Similarity	63.3%;	Pred. No. 4.5e-58;		
Matches 119;	Conservative 25;	Mismatches 39;	Indels 5;	Gaps 1.

[illegible]

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RESULT 15
US-10-307-441-19
; Sequence 19, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and Alkalophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Aspergillus awamori
; US-10-307-441-19

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Query Match	64.3%;	Score 671.5;	DB 14;	Length 189;
Best Local Similarity	65.6%;	Pred. No. 8,4e-58;		
Matches 120;	Conservative 23;	Mismatches 39;	Indels 1;	Gaps 1

Qy	7	TGHNNGYYYSFWTDGGGDVLTYNNGNAGSYSEMSNVNPFVGKGNPFSA-KDITYSGNF	65
Db	7	TGHNNGYYYSFWTDGGGDVLTYNNGNAGSYSEMSNVNPFVGKGNPFSA-KDITYSGNF	65
Qy	67	NPNGNSYLSVYGMNRNDPLIEYIVENFGTYNPSGTGATKLGVEYTSDGSYYDIYRORVNPQ	126
Db	66	TPSGNGYLSVYGMTTLPLEIYYIVESYGYNPSGSGGTGRNVSSDGSYYDIYTRNTNAP	125
Qy	127	SIIGTATFYQYMSVRNRNHSSSGSVNTANFNEMAAQGLTGMDOYIVAVGYSFGSSGAS	186
Db	126	SIGGTQFYQYMSVRQNRKRVGTVTTSNHFNMAKUGMLGTHNYQILATIGYQSSGSSS	185
Qy	187	ITV 189	
Db	186	ITI 188	

Search completed: June 30, 2004, 19:59:12
Job time : 38.25 secs

A:Reference number: S39883; MUID:94088442; PMID:8264524
A:Accession: S39883
A:Molecule type: DNA
A:Residues: 1-223 <SAA>
A:Cross-references: EMBL:S67387; NID:9455906; FIDN:AA29346.1; PID:9455907
A:Experimental source: strain QM6a
A:Accession: S39884
A:Molecule type: protein
A:Residues: 34-43;49-57;121-151;178-191 <SAF>
A:Genetics:
A:Gene: xln2
A:Introns: 91/2
A:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolyase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-33/Domain: propeptide #status predicted <PRO>
F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F:45-223/Domain: endo-1,4-beta-xylanase homology <XVL>
F:71-94/Binding site: carbohydrate (asn) (covalent) #status predicted
F:110-121/Binding site: substrate (Tyr) #status predicted
F:119,210/Active site: Glu #status predicted

Query Match 100.0%; Score 1045; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 6.8e-73;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 60
Db 34 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 93

Cy 61 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 94 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 153

Cy 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
Db 154 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 213

Cy 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 3
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N:Alternate names: xylanase IIA
C:Species: Trichoderma viride
C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
C:Accession: A44594
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44594
A:Molecule type: protein
A:Residues: 1-190 <YAG>
A:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XVL>
F:77,88/Binding site: substrate (Tyr) #status predicted
F:86,177/Active site: Glu #status predicted

Query Match 97.8%; Score 1022; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 3.3e-71;
Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Cy 1 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 60

Db 1 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 60
Cy 61 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 61 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120

Cy 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
Db 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180

Cy 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 4
A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)
N:Alternate names: xylanase IIB
C:Species: Trichoderma viride
C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
C:Accession: A44595
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44595
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-190 <YAG>
A:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XVL>
F:86,177/Active site: Glu #status predicted
F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 95.8%; Score 1005; DB 1; Length 190;
Best Local Similarity 95.8%; Pred. No. 6.5e-70;
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Cy 1 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 60
Db 1 OTTGGTGNNGYFYSYWMDHGVTYTNPGGQFVSVMNSGKGFVGGKMGQPTKXKVI 60

Cy 61 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 61 NFSGYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120

Cy 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
Db 121 QRVNOPSITIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180

Cy 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 5
A44593
endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain
N:Alternate names: xylanase
C:Species: Trichoderma harzianum
C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C:Accession: A44593
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44593
A:Molecule type: protein

A;Residues: 1-190 <YAG>
A;Experimental source: strain E58
R;Campbell, R.L.; Rose, D.R.
Submitted to the Brookhaven Protein Data Bank, June 1994
A;Reference number: A52868; PDB:1XND
A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190
C;Function:
A;Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
F;16,177/Active site: Glu #status experimental

Query Match 95.3%; Score 996; DB 1; Length 190;
Best Local Similarity 94.7%; Pred. No. 3,1e-69;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 60
DB 1 QTIQPGTGYNNNGYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 60
QY 61 NFSSSYNPNNGSYLSYVMSRNPLEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFSSSYNPNNGSYLSYVMSRNPLEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSITGATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYF 180
DB 121 QRVNQPSITGATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 6

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
C;Species: Chaetomium gracile
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
C;Accession: S71473; S78207
R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in As
A;Reference number: S71472; MUID:96118924; PMID:8595661
A;Accession: S71473
A;Molecule type: DNA
A;Residues: 1-241 <YOS>
A;Cross-references: EMBL:D49851; NID:q1339859; PDB:BA08650.1; PID:q1339860
A;Accession: S78207
A;Molecule type: Protein
A;Residues: 38-44;89-91;153-161 <YOH>
C;Genetics:
A;Intons: 88/2
C;Function:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
F;43-220/Domain: endo-1,4-beta-xylanase homology <XYL>
F;116,207/Active site: Glu #status predicted

Query Match 73.3%; Score 765.5; DB 2; Length 241;
Best Local Similarity 73.8%; Pred. No. 1.7e-51;
Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;

QY 7 TGVNNGFYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 66
DB 38 TGVNNGFYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 66
QY 67 NPNNGSYLSYVMSRNPLEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRTQVNP 126

DB 97 NPNNGSYLSYVMSRNPLEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRTQVNP 156
QY 127 SIIGTATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYFSSGSAS 186
DB 157 SIIGTATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYFSSGSAS 216
QY 187 ITV 189
DB 217 VNV 219

RESULT 7

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
N;Alternate names: xylanase A
C;Species: Chaetomium gracile
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
C;Accession: S71472; S78206
R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
Curr. Genet. 29, 73-80, 1995
A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in As
A;Reference number: S71472; MUID:96118924; PMID:8595661
A;Accession: S71472
A;Molecule type: DNA
A;Residues: 1-219 <YOS>
A;Cross-references: EMBL:D49850; NID:q1339857; PDB:BA08649.1; PID:q1339858
A;Accession: S78206
A;Molecule type: Protein
A;Residues: 31-45;82-94;152-160 <YOH>
C;Genetics:
A;Intons: 81/2
C;Function:
A;Pathway: xylan degradation
C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
F;115,206/Active site: Glu #status predicted

Query Match 67.5%; Score 705.5; DB 2; Length 219;
Best Local Similarity 68.1%; Pred. No. 5.7e-47;
Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTVNNNGFYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 65
DB 36 GTVNNNGFYFYSYVNDHGGVYTNQPGQFVSVMNSGNFVGKQMPGTRKXKI 65
QY 66 YNPNNGSYLSYVMSRNPLEYIYVENFGTNPSTGATKLGVTSDGSVYDIYRTQVNP 125
DB 95 FSPQNGYLAIVGWTQNPFLVEYIYVESFGTYDPSQAKFGTIQDDGSTYIATKTRNQ 154
QY 126 PSIIIGTATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYFSSGSAS 185
DB 155 PSIIIGTATFYQVWSVRNRSSGSVNTANHFMAAQOGLTGTMDYQIVAVGYFSSGSAS 214
QY 186 SITVS 190
DB 215 SITVS 219

RESULT 8

UC7577
endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
C;Species: Aspergillus oryzae
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
C;Accession: UC7577; PC7120
R;Kimura, T.; Suzuki, H.; Furushashi, H.; Aburatani, T.; Morimoto, K.; Sakka, S.; Sakka, Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000
A;Title: Molecular cloning, overexpression, and purification of a major xylanase from As
A;Reference number: UC7577; MUID: 21077500; PMID:11210150
A;Accession: UC7577

A:Accession: PC7086
 A:Molecule type: protein
 A:Residues: 32-51 <K12>
 C:Genetics:
 A:Gene: xylA
 A:Introns: 89/2
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match
 Best Local Similarity 62.8%; Score 656; DB 2; Length 221;
 Matches 118; Conservative 30; Mismatches 41; Indels 2; Gaps 2;

1 QTTQPG-TGVNNGFYSYNDHGGVYTNNGPGGQFVSNMNSGNFVGKMGQPGTKNKV 59
 32 QTTSSQTGNNNGYYSFMTNNGGTVOYTNAGAGSYVTWENCGDFSGKMTGSA-RD 90
 DB INFGSYNPNNGSYLSYVGSRNPLIEYIVENFGITNPSTGATKLGVTSDGSVYDIYR 119
 60 ITTEGTNPNGMAYLAVYGMTTSLVEYIYLEDYGDVNPNSMTYKGTVSDGSVYDIYE 150
 DB 91 ITTEGTNPNGMAYLAVYGMTTSLVEYIYLEDYGDVNPNSMTYKGTVSDGSVYDIYE 150
 QY 120 TORVNGSITIGATFYVNSVRNRHSSGSVNTANHFNAQAQGLITGMDYQIVAVEG 179
 DB 151 HQVNGPSISIGATFVNGVMSIRONTSSGVTYTNHFNAQAQGLITGMDYQIVAVEG 210
 QY 180 FSSGSASITVS 190
 DB 211 ESSGSSTITVS 221

RESULT 12
 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
 S43919
 C:Species: Humicola insolens
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
 C:Accession: S43919
 R:Dalboge, H.; Heldt-Hansen, H.P.
 Mol. Gen. Genet. 243, 253-260, 1994
 A:Title: A novel method for efficient expression cloning of fungal enzyme genes.
 A:Reference number: S43919; MUID:94247364; PMID:8180078
 A:Accession: S43919
 A:Molecule type: mRNA
 A:Residues: 1-227 <DNL>
 A:Cross-references: EMBL:X76047; NID:9505260; PIDN:CAA53632.1; PID:9505261
 C:Genetics:
 A:Gene: xylA
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
 F:48-225/Domain: endo-1,4-beta-xylanase homology <XVL>
 F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
 F:121,212/Active site: Glu #status predicted

Query Match
 Best Local Similarity 58.8%; Score 614.5; DB 2; Length 227;
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

8 GYNNGYFSYNDHGGVYTNNGPGGQFVSNMNSGNFVGKMGQPGTKNKVINFSSQYN 67
 DB 44 GYNNGYFSYNDHGGVYTNNGPGGQFVSNMNSGNFVGKMGQPGTKNKVINFSSQYN 67
 QY 68 PNGNSYLSYVGSNPLIEYIVENFGITNPSTGATKLGVTSDGSVYDIYRTORVNPQS 127
 DB 103 PNGNGYLAIVYGMTNPLVEYIYLEDYGDVNPNSMTYKGTVSDGSVYDIYE 162
 QY 128 ITGATFYQVNSVRNRHSSGSVNTANHFNAQAQGLITGMDYQIVAVEGSSASIT 167
 DB 163 IDGRTFTFOQVWSIRKNKRVGSSVNMNHFNAQAQGLITGMDYQIVAVEGSSASIT 222
 QY 188 TV 189

DB 223 YV 224

RESULT 13
 JS0590
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
 N:Alternate names: xylanase B
 C:Species: Streptomyces lividans
 C:Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
 C:Accession: JS0590; PS0239
 R:Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
 Gene 107, 75-82, 1991
 A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
 A:Reference number: JS0589; MUID:92077439; PMID:1743521
 A:Accession: JS0590
 A:Molecule type: DNA
 A:Residues: 1-333 <SHA>
 A:Cross-references: GB:M64552
 A:Accession: PS0239
 A:Molecule type: protein
 A:Residues: 41-71 <SH2>
 C:Genetics:
 A:Gene: xlnB
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylansidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-40/Domain: signal sequence #status predicted <SIG>
 F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
 F:54-230/Domain: endo-1,4-beta-xylanase homology <XVL>
 F:127,217/Active site: Glu #status predicted

Query Match
 Best Local Similarity 56.6%; Score 591; DB 1; Length 333;
 Matches 108; Conservative 33; Mismatches 44; Indels 16; Gaps 5;

5 PGT-----GYNNGYFSYNDHGGVYTNNGPGGQFVSNMNSGNFVGKMGQ 52
 DB 35 PGTQAQDVTVTNNGGTNNNGYYSFMTNNGGTVOYTNAGAGSYVTWENCGDFSGKMTGSA-RD 94
 QY 53 PGTAKVINFSSYNPNGSYLSYVGSRNPLIEYIVENFGITNPSTGATKLGVTSDG 112
 DB 95 NGR-RTVOYSGSFPSGNAVALYGMTNPLVEYIYLEDYGDVNPNSMTYKGTVSDG 151
 QY 113 SYVDIYRTORVNPQSIIIGATFYQVNSVRNRHSSGSVNTANHFNAQAQGLITGMD-Y 171
 DB 152 GTYDIYKTRVKNKPSVEGRTFDQYMSVRSKRTGIIITGNHFDAMRAGMPLGNFSY 211
 QY 172 QIVAVEGYSSGSASITV 189
 DB 212 MIMATEGYSSGSSTSSINV 229

RESULT 14
 TS0601
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
 N:Alternate names: xylanase B
 C:Species: Streptomyces coelicolor
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
 C:Accession: TS0601
 R:Redenbach, M.; Kleser, H.M.; Denapate, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hop
 Mol. Microbiol. 21, 77-96, 1996
 A:Title: A set of ordered cosmid and a detailed genetic and physical map for the 8 Mb
 A:Reference number: Z20556; MUID:97000351; PMID:8843436
 A:Accession: TS0601
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-335 <RED>
 A:Cross-references: EMBL:AL133220; PIDN:CAB61738.1
 A:Experimental source: strain A3(2)
 C:Genetics:

A:Gene: xlnB
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase

Query Match 56.6%; Score 591; DB 2; Length 335;
Best Local Similarity 55.1%; Pred. No. 5.2e-38;
Matches 109; Conservative 31; Mismatches 42; Indels 16; Gaps 5;

Search completed: June 30, 2004, 19:41:13
Job time : 14 secs

QY 5 PGT-----GYNNGYFYSMNDGCGVTYTNPGGQFSPVMSNSGNFVGGKQW 52
DB 36 PGTAGADTVTTNTEGNTNGYFYFMTDSQGTVMNMGSGQYSTNRTGNFVAGKGA 95
QY 53 PGTNNKVINPFGSYNPNNGNSLYVYGSRNPLIEYIVENFGTYNPGTATKLGCVTSDG 112
DB 96 NGGR-RTVQYSGSFNPGNAYLALYGTWSNPLVEYIVDMWGTYP-TGEYK-GTVTSDG 152
QY 113 SVYDIYRTQVNPQSIIGTATFFVQYMSVRNHRSSGSVNTANFNMAAQGLTLGTM-D-Y 171
DB 153 GTYDIYKTRVKNKPSVEGRTFPOQYMSVRQAKRTGTTGNHFDMAKAPLGNFSY 212
QY 172 QIVAVEGYFSSGSASITV 189
DB 213 MIVATEGYQSSGSSSINV 230

RESULT 15

140712
endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi
N:Alternate names: xylanase D
C:Species: Cellulomonas fimi
C>Date: 16-Aug-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999
C:Accession: 140712
R:Milward-Sadler, S.J.; Poole, D.M.; Henrissat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilh
Mol. Microbiol. 11, 375-382, 1994
A:Title: Evidence for a general role for high-affinity non-catalytic cellulose binding d
A:Reference number: 140712; MUID:9422415; PMID:8170399
A:Accession: 140712
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-644 <RES>
A:Cross-references: EMBL:X76729; NID:9558176; PIDN:CA54145.1; PID:9558177
C:Genetics:
A:Gene: xynD
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xyloisidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology; r
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-35/Domain: signal sequence #status predicted <SIG>
F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <MAT>
F:361-508/Domain: nodB homology <NODB>
F:126,216/Active site: Glu #status predicted

Query Match 55.1%; Score 575.5; DB 1; Length 644;
Best Local Similarity 55.7%; Pred. No. 1.7e-36;
Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGVNNGYFYSMNDGCGVTYTNPGGQFSPVMSNSGNFVGGKQWPGTKNKNYINFGSY 66
DB 49 TGTHDGYFYFMTDSQGTVMNMGSGQYSTNRTGNFVAGKGA 106
QY 67 NPNNGSYLYSVYGSRNPLIEYIVENFGTYNPGTATKLGCVTSDGSVDYVTRQVNP 126
DB 107 NPSNAYLTLGYQSLVEYIVDSKGTYP--GTFMGTVTSDGTYDIYRTQVKNP 164
QY 127 SIIG-TATFYQYMSVRNHRSSGSVNTANFNMAAQGLTLGTM-DYIVAVEGYFSSGSA 185
DB 165 SIEDSSSTFYQYMSVRQAKRTGTTGNHFDMAKAGMNLGRHNYMIVATEGYQSSGSS 224
QY 186 SITVS 190
DB 225 SITVS 229

Fri Jul 2 14:30:07 2004

US-09-856-025B-16.rai

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds
(without alignments)
700.638 Million cell updates/sec

Title: US-09-856-025B-16

Perfect score: 1045
Sequence: 1 OTIQPGCGNNGYFYSYWN.....YQIVAVGGRSSGSASITVS 190

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued Patents AA.*
2: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6A COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	190	1	US-08-044-621D-26
2	1045	100.0	190	1	US-08-709-912-16
3	1045	100.0	190	2	US-08-047-370-16
4	1045	100.0	223	2	US-08-121-436A-2
5	1040	99.5	190	4	US-09-570-856B-22
6	1035	99.0	190	1	US-08-709-912-17
7	1035	99.0	190	2	US-09-047-370-17
8	1032	98.8	190	1	US-08-044-621D-27
9	1022	97.8	190	4	US-09-570-856B-19
10	1016	97.2	223	3	US-08-254-733-7
11	996	95.3	190	1	US-08-044-621D-28
12	996	95.3	190	1	US-08-709-912-14
13	996	95.3	190	2	US-09-047-370-14
14	990	94.7	190	4	US-09-570-856B-20
15	721.5	69.0	261	3	US-08-768-373-2
16	721.5	69.0	261	4	US-09-849-242A-2
17	676.5	64.7	225	4	US-09-570-856B-26
18	665.5	63.7	225	1	US-08-290-979A-8
19	656.5	62.8	230	3	US-08-768-373-4
20	656.5	62.8	230	4	US-09-849-242A-4
21	650.5	62.2	221	4	US-09-570-856B-29
22	647.5	62.0	223	4	US-09-462-246-2
23	640	61.2	226	4	US-09-367-891A-2
24	635.5	60.8	225	2	US-08-886-765-2
25	635.5	60.8	225	3	US-09-115-660-2
26	630.5	60.3	194	4	US-09-570-856B-24
27	630	60.3	231	2	US-08-902-655A-6

28	630	60.3	226	1	US-08-507-431-6	Sequence 6, Appl
29	630	60.3	226	3	US-09-116-622-6	Sequence 6, Appl
30	630	60.3	226	3	US-09-219-277-6	Sequence 6, Appl
31	630	60.3	226	3	US-09-599-661-6	Sequence 6, Appl
32	623.5	59.7	194	4	US-09-570-856B-23	Sequence 23, Appl
33	620.5	59.4	189	1	US-08-458-025B-4	Sequence 4, Appl
34	607.5	58.1	189	1	US-08-709-912-13	Sequence 13, Appl
35	607.5	58.1	189	2	US-09-047-370-13	Sequence 2, Appl
36	595.5	57.0	344	4	US-08-468-812-2	Sequence 2, Appl
37	595.5	57.0	344	4	US-08-590-563-2	Sequence 2, Appl
38	595.5	57.0	344	4	US-09-770-621-2	Sequence 2, Appl
39	595.5	57.0	344	4	US-09-235-832-2	Sequence 2, Appl
40	591	56.6	206	1	US-08-315-695-19	Sequence 19, Appl
41	591	56.6	215	1	US-08-044-621D-34	Sequence 34, Appl
42	591	56.6	335	4	US-09-570-856B-15	Sequence 15, Appl
43	589	56.4	191	1	US-08-709-912-10	Sequence 10, Appl
44	589	56.4	191	2	US-09-047-370-10	Sequence 10, Appl
45	565.5	54.1	197	1	US-08-044-621D-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-044-621D-26
Sequence 26, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Ming L. Sung
APPLICANT: Makoto Yasuguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSER: Gowing, Strathly & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1G3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Tortorene, A., Mach, R. L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.,
AUTHORS: & Kudicek, C. P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGSGVYTNPGGQFSYVMSNSGNFVGKGMQPTKXVI 60
DB 1 QTIQPGTGYNNGYFYSYNDGSGVYTNPGGQFSYVMSNSGNFVGKGMQPTKXVI 60
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGYNSGTATKLGCVTSVDSYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGYNSGTATKLGCVTSVDSYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTANHFNMAOQGLTLGTMDOYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTANHFNMAOQGLTLGTMDOYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: XYN II
PUBLICATION INFORMATION:
AUTHORS: Tortorene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kudicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 100.0%; Score 1045; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;
Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGSGVYTNPGGQFSYVMSNSGNFVGKGMQPTKXVI 60
DB 1 QTIQPGTGYNNGYFYSYNDGSGVYTNPGGQFSYVMSNSGNFVGKGMQPTKXVI 60
QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGYNSGTATKLGCVTSVDSYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGYNSGTATKLGCVTSVDSYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTANHFNMAOQGLTLGTMDOYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRRNRSSGSVNTANHFNMAOQGLTLGTMDOYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-15
Sequence 16, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047.370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 100.0%; Score 1045; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.2e-89;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWNDHGQGVYTYNGPGQFVSVMNSGNYFGKGMQPGTKNKVI 60
DB 1 QTIQPGTYNNGYFYSYWNDHGQGVYTYNGPGQFVSVMNSGNYFGKGMQPGTKNKVI 60
QY 61 NFGSYVNPNGSYLSYVGMSENPFLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFGSYVNPNGSYLSYVGMSENPFLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQWYVRNRHSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQWYVRNRHSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Riitta
APPLICANT: Paloheimo, Marja
APPLICANT: Lahtinen, Tarja
APPLICANT: Pajerster w, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Keesler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 100.0%; Score 1045; DB 2; Length 223;
Best Local Similarity 100.0%; Pred. No. 1.5e-89;

Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWNDHGQGVYTYNGPGQFVSVMNSGNYFGKGMQPGTKNKVI 60
DB 34 QTIQPGTYNNGYFYSYWNDHGQGVYTYNGPGQFVSVMNSGNYFGKGMQPGTKNKVI 93
QY 61 NFGSYVNPNGSYLSYVGMSENPFLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
DB 61 NFGSYVNPNGSYLSYVGMSENPFLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQWYVRNRHSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQWYVRNRHSSGSVNTANHFNAQAQGLTLGTMQYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 223

RESULT 5
US-09-570-856B-22

Sequence 22, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Bahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-22

Query Match
Best Local Similarity 99.5%; Score 1040; DB 4; Length 190;
Best Local Similarity 100.0%; Pred. No. 3.6e-89;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTGPTGYNNGYFYSYVMDHGCVTTNGPGGQFSVNMNSGNFVGKGMQPGTKNXYIN 61
DB 2 TTGPTGYNNGYFYSYVMDHGCVTTNGPGGQFSVNMNSGNFVGKGMQPGTKNXYIN 61
QY 62 FSGSYVNPNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKGEVTSDSGYVDIYRTQ 121
DB 62 FSGSYVNPNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKGEVTSDSGYVDIYRTQ 121
QY 122 RVNQPSIIIGTATFYQYWSYVRNHRSSGSVNTANHNMAAQQGLTGTMDYQIVAVEGYF 181
DB 122 RVNQPSIIIGTATFYQYWSYVRNHRSSGSVNTANHNMAAQQGLTGTMDYQIVAVEGYF 181
QY 182 SSGSASITVS 190
DB 182 SSGSASITVS 190

RESULT 6
US-08-709-912-17
Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Ieguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujle, M
AUTHORS: Watson, D. C.
AUTHORS: Makarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match
Best Local Similarity 98.9%; Score 1035; DB 1; Length 190;
Best Local Similarity 98.9%; Pred. No. 1.1e-88;
Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTTPGTGYNNGYFYSYVMDHGCVTTNGPGGQFSVNMNSGNFVGKGMQPGTKNXYI 60
DB 1 QTTPGTGYNNGYFYSYVMDHGCVTTNGPGGQFSVNMNSGNFVGKGMQPGTKNXYI 60
QY 61 NPSGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKGEVTSDSGYVDIYRT 120
DB 61 NPSGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKGEVTSDSGYVDIYRT 120
QY 121 QRVNQPSIIIGTATFYQYWSYVRNHRSSGSVNTANHNMAAQQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNQPSIIIGTATFYQYWSYVRNHRSSGSVNTANHNMAAQQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Ieguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/047,370
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/709,912
 FILING DATE: 09-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Olisen M., Warren E.
 REGISTRATION NUMBER: 27290
 REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma viride
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi, M
 AUTHORS: Roy, C
 AUTHORS: Ujile, M
 AUTHORS: Watson, D. C.
 AUTHORS: Makarchuk, W.
 JOURNAL: Xylan and Xylanase
 PAGES: 149-154
 DATE: 1992
 US-09-047-370-17

Query Match 99.8%; Score 1035; DB 2; Length 190;
 Best Local Similarity 98.9%; Pred. No. 1.1e-88;
 Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QTIQPGTGNNGYRYSYWNDSHGVTYTNPGGQFSYVWNSGNTFVGKGMQPGTKNKVI 60
 Db 1 QTIQPGTGNNGYRYSYWNDSHGVTYTNPGGQFSYVWNSGNTFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEIYYIYENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSYVGWSRNPLEIYYIYENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQWASVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQWASVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180
 QY 181 SSGSASTTYS 190
 Db 181 SSGSASTTYS 190

RESULT 8
 US-08-044-621D-27
 Sequence 27, Application US/08044621D
 Patent No. 5405769
 GENERAL INFORMATION:
 APPLICANT: Warren W. Makarchuk
 APPLICANT: Wing L. Sung
 APPLICANT: Makoto Yaguchi
 APPLICANT: Robert L. Campbell
 APPLICANT: David R. Rose
 TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strathy & Henderson
 STREET: Suite 2600, 160 Elgin Street
 CITY: Ottawa
 STATE: Ontario
 COUNTRY: Canada
 ZIP: K1P 1C3
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/044,621D
 FILING DATE: April 8, 1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Judy A. Eriault
 REGISTRATION NUMBER: 34,076
 REFERENCE/DOCKET NUMBER: 08-863796
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 613-786-0199
 TELEFAX: 613-563-9869
 TELEX:
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190
 TYPE: Amino Acid
 STRANDEDNESS: No. 5405769 Relevant
 TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: NO
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma viride
 STRAIN: Trichoderma viride, 20kD
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
 AUTHORS: D.C. & Makarchuk W.
 TITLE: Amino Acid Sequence of the Low-Molecular-
 TITLE: Weight Xylanase from Trichoderma viride
 JOURNAL: Xylans and Xylanases
 VOLUME:
 ISSUE:
 PAGES: 149-154
 DATE: 1992
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-27

Query Match 98.8%; Score 1032; DB 1; Length 190;
 Best Local Similarity 98.4%; Pred. No. 2e-88;
 Matches 187; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QTIQPGTGNNGYRYSYWNDSHGVTYTNPGGQFSYVWNSGNTFVGKGMQPGTKNKVI 60
 Db 1 QTIQPGTGNNGYRYSYWNDSHGVTYTNPGGQFSYVWNSGNTFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSYVGWSRNPLEIYYIYENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSYVGWSRNPLEIYYIYENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQWASVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQWASVRNRHSSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180

Db 121 QVNPDSITGATFYQWYSVRTRHSSGSVNTANHFNAQAQGLTGIMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 9

US-09-570-856B-19
 ; Sequence 19, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzen, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570,856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133,714
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Trichoderma viride
 US-09-570-856B-19

Query Match 97.8%; Score 1022; DB 4; Length 190;
 Best Local Similarity 97.4%; Pred. No. 1,7e-87;
 Matches 185; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNNGYFYSYVNDGSGVYTYNNGPGQPSVYVNSGNGFVGKGMQGTNRKVI 60
 Db 1 OTIOPGTGYNNGYFYSYVNDGSGVYTYNNGPGQPSVYVNSGNGFVGKGMQGTNRKVI 60
 QY 61 NFSGTYNNGNSYLSYVGMNRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 Db 61 NFSGTYNNGNSYLSYVGMNRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 QY 121 QVNPDSITGATFYQWYSVRTRHSSGSVNTANHFNAQAQGLTGIMDYQIVAVEGYF 180
 Db 121 QVNPDSITGATFYQWYSVRTRHSSGSVNTANHFNAQAQGLTGIMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 10

US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ; GENERAL INFORMATION:
 ; APPLICANT: MATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORU
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: KIRAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE cgh1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; FILE REFERENCE: 99-0266*/LC(MMC)/00144
 ; CURRENT APPLICATION NUMBER: US/09/254,733
 ; CURRENT FILING DATE: 1999-05-07
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1
 US-09-254-733-7

Query Match 97.2%; Score 1016; DB 3; Length 223;
 Best Local Similarity 96.8%; Pred. No. 7,6e-87;
 Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNNGYFYSYVNDGSGVYTYNNGPGQPSVYVNSGNGFVGKGMQGTNRKVI 60
 Db 34 OTIOPGTGYNNGYFYSYVNDGSGVYTYNNGPGQPSVYVNSGNGFVGKGMQGTNRKVI 93
 QY 61 NFSGTYNNGNSYLSYVGMNRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 Db 94 NFSGTYNNGNSYLSYVGMNRNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 153
 QY 121 QVNPDSITGATFYQWYSVRTRHSSGSVNTANHFNAQAQGLTGIMDYQIVAVEGYF 180
 Db 154 QVNPDSITGATFYQWYSVRTRHSSGSVNTANHFNAQAQGLTGIMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 11

US-08-044-621D-28
 ; Sequence 28, Application US/08044621D
 ; Patent No. 5405769

GENERAL INFORMATION:

APPLICANT: Warren W. Makarchuk
 APPLICANT: Ming L. Sung
 APPLICANT: Makoto Yaguchi
 APPLICANT: Robert L. Campbell
 APPLICANT: David R. Rose
 TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Gwilling, Strathly & Henderson
 STREET: Suite 2600, 160 Bloor Street
 CITY: Ottawa
 STATE: Ontario
 COUNTRY: Canada

ZIP: K1P 1C3
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 COMPUTER: IBM PC
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/044,621D
 FILING DATE: April 8, 1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Judy A. Erratt
 REGISTRATION NUMBER: 34,076
 REFERENCE/DOCKET NUMBER: 08-863796
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 613-786-0199
 TELEFAX: 613-563-9869

TELEX:
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190
 TYPE: Amino Acid
 STRANDEDNESS: No. 5405769 Relevant
 TOPOLOGY: linear

MOLECULE TYPE: protein
 DESCRIPTION: protein
 HYPOTHETICAL: No
 ANTI-SENSE: No
 FRAGMENT TYPE: No
 ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum
 STRAIN: Trichoderma harzianum, 20kD
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
 AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
 TITLE: J.N.
 JOURNAL: Xylans and Xylanases
 VOLUME:
 ISSUE:
 PAGES: 435-438
 DATE: 1992
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;
 Best Local Similarity 94.7%; Pred. No. 4,4e-85;
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSSVWMDHGVYTTNGPGGPFVWMSNGNFVGGKMGQPGTKNKVI 60
 DB 1 QTIQPGTGYSSNGYYSVWMDHAGVYTTNGGGGFTVWMSNGNFVGGKMGQPGTKNKVI 60
 QY 61 NFSGSYNPENGNSYLSVYGMNRNPLIEYIVENFGTYNPGTATGCGVTSDGSVYDIYRT 120
 DB 61 NFSGSYNPENGNSYLSVYGMNRNPLIEYIVENFGTYNPGTATGCGVTSDGSVYDIYRT 120
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 12
 US-08-709-912-14
 Sequence 14, Application US/08709912
 Patent No. 5759840

GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L.
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr, Warren E
 REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma harzianum
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi, M.
 AUTHORS: Roy, C.
 AUTHORS: Watson, D. C.
 AUTHORS: Rollin, F.
 AUTHORS: Tan, L. U. L.
 AUTHORS: Senior, D. J.
 AUTHORS: Saddler, J. N.
 JOURNAL: Xylan and Xylanase
 PAGES: 435-438
 DATE: 1992
 US-08-709-912-14

Query Match 95.3%; Score 996; DB 1; Length 190;
 Best Local Similarity 94.7%; Pred. No. 4,4e-85;
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSSVWMDHGVYTTNGPGGPFVWMSNGNFVGGKMGQPGTKNKVI 60
 DB 1 QTIQPGTGYSSNGYYSVWMDHAGVYTTNGGGGFTVWMSNGNFVGGKMGQPGTKNKVI 60
 QY 61 NFSGSYNPENGNSYLSVYGMNRNPLIEYIVENFGTYNPGTATGCGVTSDGSVYDIYRT 120
 DB 61 NFSGSYNPENGNSYLSVYGMNRNPLIEYIVENFGTYNPGTATGCGVTSDGSVYDIYRT 120
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAOQGLTGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 13
 US-09-047-370-14
 Sequence 14, Application US/09047370
 Patent No. 5866408

GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L.
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F. D.
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match 95.3%; Score 996; DB 2; Length 190;
Best Local Similarity 94.7%; Pred. No. 4.4e-85;
Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTIQPGCYNNNGYVSYVWMDHGGVTTNPGGQFSYVWNSGKFGVGGKMGQPTKXKVI 60
DB 1 QTIGGTGYSNGYYSYVNDHAGAVTTNNGGGSFTVWNSGKFGVGGKMGQPTKXKVI 60
QY 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
DB 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
QY 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahljat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

Query Match 94.7%; Score 990; DB 4; Length 190;
Best Local Similarity 94.2%; Pred. No. 1.6e-84;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTIQPGCYNNNGYVSYVWMDHGGVTTNPGGQFSYVWNSGKFGVGGKMGQPTKXKVI 60
DB 1 QTIGGTGYSNGYYSYVNDHAGAVTTNNGGGSFTVWNSGKFGVGGKMGQPTKXKVI 60
QY 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
DB 61 NFSGSYNNGNSYLSIVGWSNPLIEYIVENFGTYPNPGTATLGEVTSDDGYDIYRT 120
QY 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSITGATFYQVSVRRNRSSGSVNTANHFNAHQOGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALCHIMO, MARIA
APPLICANT: HAKOLA, SATU
APPLICANT: M NYL, ARJA
APPLICANT: VEHMANPER, JARI
APPLICANT: LANTTO, RAJVA
APPLICANT: LAHTINEN, TARIJA
APPLICANT: RAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CINEBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
 TELEFAX: (202) 371-2540
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 261 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Chaetomium thermophilum
 STRAIN: CBS730.95
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..261
 OTHER INFORMATION: /label= XLNA
 US-08-768-373-2

Query Match 69.0%; Score 721.5; DB 3; Length 261;
 Best Local Similarity 65.8%; Pred. No. 2.1e-59;
 Matches 125; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 1 QTI-QPGTGNNGYFFYSYNDGSGVYTNPGGQFSYWNMSNGNPFYGGKMGQPGTKNKY 59
 Db 27 QTLTSATGTHNGYYSFWTDGQGNIRENLESQQYSVTWGNGNWYGGKMNPGTDNRV 86
 QY 60 INFSGSYNPNNGNSLYSYGMSRNPLIEYTYVENFGTYNPSGTATKLGVTSDGSVDIYR 119
 Db 87 INYADYRPNNGNSLYAVYGMTRNPLIEYVVSFGTYDPSTGATRMGSVTTDGGTYNIYR 146
 QY 120 TORVYOPSIIIGTATFYQYASVRRNHRSSGSVNTANHFNAWQGLTGMDOYQIVAVEGY 179
 Db 147 TORVYAPSIIEGKTFYQYASVRYTRSKRTGGTYTANHFNAWRQGLGSHDYQIVATEGY 206
 QY 180 FSSGSASITV 189
 Db 207 YSSGSATVNV 216

Search completed: June 30, 2004, 19:44:47
 Job time : 15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 / Search time 7.25 Seconds
(without alignments)
1364.597 Million cell updates/sec

Title: US-09-856-025B-16

Perfect score: 1045
Sequence: 1 QTIQPTGTYNNGYFSYMD.....YQIVAVGYPSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	100.0	222	1	XYN2_TRIRE
2	990	94.7	190	1	XYN1_TRIA
3	684.5	65.5	225	1	XYN1_EMEI
4	676.5	64.7	225	1	XYN2_ASPIA
5	670.5	64.2	221	1	XYN2_EMEI
6	664.5	63.6	225	1	XYN2_ASPIA
7	650.5	62.2	221	1	XYN1_COCA
8	635.5	60.8	225	1	XYN1_THBA
9	614.5	58.8	227	1	XYN1_HUMI
10	594	56.8	335	1	XYN2_STRI
11	575.5	55.1	644	1	XYN2_CELFI
12	571.5	54.7	233	1	XYN2_MAGR
13	565.5	54.1	197	1	XYN1_SCHC
14	527	50.4	240	1	XYN1_STRI
15	525.5	50.3	210	1	XYN1_BACST
16	503	48.1	213	1	XYN1_BACST
17	502	48.0	213	1	XYN1_BACCI
18	461	44.1	228	1	XYN1_BACPU
19	453.5	43.4	261	1	XYN1_CLOS
20	444	42.5	512	1	XYN1_CLOS
21	442.5	42.3	229	1	XYN1_TRIE
22	430	41.1	211	1	XYN1_ASPIA
23	430	41.0	211	1	XYN1_ASPIA
24	428	41.1	211	1	XYN1_ASPIA
25	425	40.7	211	1	XYN1_ASPIA
26	402	38.5	954	1	XYN1_ASPIA
27	383.5	36.7	802	1	XYN1_ASPIA
28	373.5	35.7	179	1	XYN1_PSEXY
29	305	29.2	607	1	XYN1_NEOPA
30	286.5	27.4	608	1	XYN1_FIBSU
31	246	23.5	625	1	XYN1_FIBSU
32	98.5	9.4	159	1	GRPA_MEDFA
33	98	9.4	414	1	PHAI_PSELE

SUMMARIES

ALIGNMENTS

RESULT 1.
ID XYN2_TRIRE STANDARD; PRT; 222 AA.
AC P36217;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
DE (1,4-beta-D-xylan xylanohydrolase 2).
GN XYN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_Taxid=51453;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN=C30;
RC MEDLINE=93103679; PubMed=1369024;
RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,
RT Harkki A., Kubicek C.P.,
RT "The two major xylanases from Trichoderma reesei: characterization of
both enzymes and genes.",
RL Biotechnology 10:1461-1465(1992).
RN (2)
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RP STRAIN=C30;
RC MEDLINE=94283373; PubMed=8013449;
RA Toerrien A., Harkki A., Rouvinen J.,
RT "Three-dimensional structure of endo-1,4-beta-xylanase II from
Trichoderma reesei: two conformational states in the active site.",
RL EMBO J. 13:2493-2501(1994).
RN (3)
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RP STRAIN=C30;
RC MEDLINE=95127663; PubMed=7827044;
RA Toerrien A., Rouvinen J.,
RT "Structural comparison of two major endo-1,4-xylanases from
Trichoderma reesei.",
RL Biochemistry 34:847-856(1995).
RN (4)
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RP STRAIN=C30;
RC MEDLINE=96502263; PubMed=8755744;
RA Havukainen R., Toerrien A., Laitinen T., Rouvinen J.,
RT "Covalent binding of three epoxalyxyl xylosides to the active site of
endo-1,4-xylanase II from Trichoderma reesei.",
RL Biochemistry 35:9617-9624(1996).
CC -1- CARBHYLIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
hydrolases).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sb-sib.ch).

CC ENBL; X69573; CAA49293.1; -.
 DR PIR; S39154; S39154.
 DR PDB; 1XYP; 08-AUG-95.
 DR PDB; 1XYP; 08-AUG-95.
 DR PDB; 1ENX; 08-AUG-95.
 DR PDB; 1RED; 11-JAN-97.
 DR PDB; 1RED; 11-JAN-97.
 DR PDB; 1RED; 11-JAN-97.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
 KM 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 33 222
 FT ACT_SITE 118 118
 FT ACT_SITE 209 209
 FT CARBOHYD 70 70
 FT CARBOHYD 93 93
 FT CARBOHYD 129 129
 FT STRAND 34 35
 FT STRAND 38 42
 FT STRAND 43 44
 FT STRAND 45 51
 FT STRAND 57 61
 FT STRAND 64 65
 FT TURN 66 71
 FT STRAND 66 71
 FT STRAND 76 83
 FT STRAND 91 101
 FT STRAND 104 113
 FT TURN 114 116
 FT STRAND 117 125
 FT TURN 130 133
 FT STRAND 135 142
 FT TURN 143 144
 FT STRAND 145 157
 FT TURN 160 161
 FT STRAND 164 173
 FT STRAND 180 183
 FT HELIX 184 193
 FT TURN 194 195
 FT STRAND 200 211
 FT STRAND 214 222
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963BF CRC64;

Query Match 100.0%; Score 1045; DB 1; Length 222;
 Best Local Similarity 100.0%; Pred. No. 3, 1e-76;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGYFYSYNNNDGAGVYTNBPGQFYSYNNNSGNGFVGKGMQPGTKXKVI 60
 DB 33 QTIQGTGNNNGYFYSYNNNDGAGVYTNBPGQFYSYNNNSGNGFVGKGMQPGTKXKVI 92
 QY 61 NFSGSYNNNGSYLSYVGMKRNPLIEYIVENFGTVNPSGCATLGEVTSQGSYYDIYRT 120
 DB 93 NFSGSYNNNGSYLSYVGMKRNPLIEYIVENFGTVNPSGCATLGEVTSQGSYYDIYRT 152
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNMAQGGTLTGMDYQIYAVEGYF 180
 DB 153 QRVNOPSIIIGTATFYQYWSVRNRHSSGVSNTANHFNMAQGGTLTGMDYQIYAVEGYF 212
 QY 181 SSGSASTIVS 190
 DB 213 SSGSASTIVS 222

RESULT 2

AC P48793;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 DE xylanohydrolase).
 OS Trichoderma harzianum.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; Hypocreales; Hypocrea.
 OX NCBI_Taxid=5544;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=E58;
 RA Vaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
 RA Sadtler J.N.;
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
 RT harzianum E58.";
 RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,
 RL Voregen A.G.J. (eds.);
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,
 RA Vaguchi M.;
 RT "High-resolution structures of xylanases from B.circulans and
 RT T.harzianum identify a new folding pattern and implications for the
 RT atomic basis of the catalysis.";
 RL (In) Suominen P., Reinikainen T. (eds.);
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,
 RL Foundation for Biotechnical and Industrial Fermentation Research,
 RL Helsinki (1993).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylansidic
 CC linkages in xylans.
 CC -!- PATHWAY: Xylan degradation.
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC PDB; 1XND; 20-DEC-94.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; 3D-structure.
 FT ACT_SITE 86 86
 FT ACT_SITE 177 177
 FT STRAND 3 3
 FT STRAND 6 9
 FT STRAND 14 19
 FT STRAND 25 29
 FT TURN 32 33
 FT STRAND 34 39
 FT STRAND 44 51
 FT TURN 56 57
 FT STRAND 59 69
 FT STRAND 72 81
 FT TURN 82 84
 FT STRAND 85 93
 FT TURN 98 101
 FT STRAND 103 110
 FT TURN 111 112
 FT STRAND 113 125
 FT TURN 128 129
 FT STRAND 132 141
 FT STRAND 148 151
 FT HELIX 152 163
 FT TURN 162 163
 FT STRAND 166 179

FT STRAND 182 190
SQ SEQUENCE 190 AA; 20703 MW; 6A0FAD1C3599C698 CRC64;
Query Match 94.7%; Score 990; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 7, 7e-74;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTIPGGYNNNGYRYSWNDGGVYTNNGPGGQFVSVMNSGNGFVGGKMGQPGTKNKV 60
DB 1 OTIPGGYNNNGYRYSWNDGGVYTNNGPGGQFVSVMNSGNGFVGGKMGQPGTKNKV 60
QY 61 NFSGSYNNPNSYLSYVGMNSNPPIEYIVENFGTYNPSTGATKLGCVTSDDGVYDIYRT 120
DB 61 NFSGSYNNPNSYLSYVGMNSNPPIEYIVENFGTYNPSTGATKLGCVTSDDGVYDIYRT 120
QY 121 QRVNPPSTIGATFYQVWSVRNRSSGSVNTAHNFMAAQGLTLGTMQYIVAVEGYF 180
DB 121 QRVNPPSTIGATFYQVWSVRNRSSGSVNTAHNFMAAQGLTLGTMQYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XYN1 EMBL STANDARD; PRT; 225 AA.
ID XYN1 EMBL STANDARD; PRT; 225 AA.
AC P55332; 000173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylan xylanohydrolase 1).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
RX MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182 (1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC
DR EMBL; Z49892; CA90073.1; -.
DR PIR; S57477; S57477.
DR HSSP; P48793; 1XND.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco hydro 11.
DR Pfam; PF00457; Glyco hydro 11; 1.
DR PRINTS; PR0911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 19
FT CHAIN 20 225
FT ACT_SITE 121 121
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7EBC CRC64;

Query Match 65.5%; Score 684.5; DB 1; Length 225;
Best Local Similarity 66.1%; Pred. No. 6, 6e-49;
Matches 121; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGVNNEFYSYNNNDGGVYTNNGPGGQFVSVMNSGNGFVGGKMGQPGTKNKV 66
DB 43 TGVNNEFYSYNNNDGGVYTNNGPGGQFVSVMNSGNGFVGGKMGQPGTKNKV 66
QY 67 NFSGSYNNPNSYLSYVGMNSNPPIEYIVENFGTYNPSTGATKLGCVTSDDGVYDIYRT 126
DB 102 NFSGSYNNPNSYLSYVGMNSNPPIEYIVENFGTYNPSTGATKLGCVTSDDGVYDIYRT 126
QY 127 SIIGTTFEYQVWSVRNRSSGSVNTAHNFMAAQGLTLGTMQYIVAVEGYF 186
DB 162 SIIGTTFEYQVWSVRNRSSGSVNTAHNFMAAQGLTLGTMQYIVAVEGYF 186
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
XYNB ASPKA STANDARD; PRT; 225 AA.
ID XYNB ASPKA STANDARD; PRT; 225 AA.
AC P48824;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XYNB.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=40384;
RX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4308;
RA Ito K.;
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC
DR EMBL; D38070; BAA07264.1; -.
DR HSSP; P36217; 1XTO.
DR InterPro; IPR008985; ConA like lec g1.
DR InterPro; IPR001137; Glyco hydro 11.
DR Pfam; PF00457; Glyco hydro 11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 225
FT ACT_SITE 121 121
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match 64.7%; Score 676.5; DB 1; Length 225;
Best Local Similarity 66.1%; Pred. No. 3e-48;
Matches 121; Conservative 23; Mismatches 38; Indels 1; Gaps 1;

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QY 7 TGYNNGYFYSYWMDHGCVTYTNGPGGQFSVWNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 43 TGENNGFYYSFWTDDGGDVYTYTNGNAGSYSEVMSVNGNPFVGGKMGWPSA-KDITVSGNF 101
QY 67 NPNKNSYLSVYGSRNPLIEYIYVENGTNPSTGATKGEVPSDGSVDYRTQRPVNP 126
DB 102 TPGSGNGLSYGWTNPLIEYIYVESYGDYVNPSCGCTTKNGVNSDDSYVDIYATPTNP 161
QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 186
DB 162 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 221
QY 187 ITVS 189
DB 222 ITI 224

RESULT 5
XYN2_EMENT STANDARD; PRT; 221 AA.
ID XYN2_EMENT
AC P55333; Q00176;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
OS Emericella nidulans (Aspergillus nidulans)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=96236210; PubMed=8787417;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes."
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; 249893; CA90074.1; -.
CC DR PIR; S57469; S57469.
CC DR HSSP; P48793; 1XND.
CC DR InterPro; IPR008985; ConA_like lec g1.
CC DR InterPro; IPR001137; Glyco_hydro_11.
CC DR Pfam; PF00457; Glyco_hydro_11; 1.
CC DR PRINTS; PR00911; GLHYDRLASE11.
CC DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC DR Xylan degradation; Hydrolase; Glycosidase; Signal.
CC KW CHAIN 1
CC FT SIGNAL 18
CC FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.
CC FT ACT SITE 117 117 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT SITE 208 208 PROTON DONOR (BY SIMILARITY).
CC FT ACT SITE 208 208 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 221 AA; 23517 MW; 42665B5E80DDE9475 CRC64;

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Query Match 64.2%; Score 670.5; DB 1; Length 221;
Best Local Similarity 65.8%; Pred. No. 8.9e-48;
Matches 121; Conservative 26; Mismatches 36; Indels 1; Gaps 1;
QY 7 TGYNNGYFYSYWMDHGCVTYTNGPGGQFSVWNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 43 TGENNGFYYSFWTDDGGDVYTYTNGNAGSYSEVMSVNGNPFVGGKMGWPSA-KDITVSGNF 101

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DB 39 TGTSGGYYSFWTDDGGDVYTYTNGDGSYVETKVGNFVGGKMGWPSA-SQITVSGSF 97
QY 67 NPNKNSYLSVYGSRNPLIEYIYVENGTNPSTGATKGEVPSDGSVDYRTQRPVNP 126
DB 98 IPEGNGYLSVYGSRNPLIEYIYVESYGDYVNPSCGCTTKNGVNSDDSYVDIYATPTNP 157
QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 186
DB 158 SIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGMDYQIVAVEGYFSSGSAS 217
QY 187 ITVS 190
DB 218 ITVS 221

RESULT 6
XYN2_ASPNG STANDARD; PRT; 225 AA.
ID XYN2_ASPNG
AC P55330; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
OS Emericella nidulans (Aspergillus nidulans)
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=IFO 4066;
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RL Ito K.;
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
CC DR EMBL; D38071; BA07265.1; -.
CC DR HSSP; P09850; 1XNB.
CC DR InterPro; IPR008985; ConA_like lec g1.
CC DR InterPro; IPR001137; Glyco_hydro_11.
CC DR Pfam; PF00457; Glyco_hydro_11; 1.
CC DR PRINTS; PR00911; GLHYDRLASE11.
CC DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC DR Xylan degradation; Hydrolase; Glycosidase; Signal.
CC KW CHAIN 1
CC FT SIGNAL 18
CC FT CHAIN 19 37 ENDO-1,4-BETA-XYLANASE II.
CC FT ACT SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 225 AA; 24057 MW; C4B8B8007AB2B8FD CRC64;

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Query Match 63.6%; Score 664.5; DB 1; Length 225;
Best Local Similarity 65.6%; Pred. No. 2.8e-47;
Matches 120; Conservative 22; Mismatches 40; Indels 1; Gaps 1;
QY 7 TGYNNGYFYSYWMDHGCVTYTNGPGGQFSVWNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 43 TGENNGFYYSFWTDDGGDVYTYTNGDAGAYTVWMSVNGNFVGGKMGWPSA-D-ITVSGTF 101

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Qy	67	NPENNSLSTSYGMSRPMLEEVYIVENFTGYNSTATKLGEVTSQSVYDIYRTQRYNOCP	126
Db	102	TPSGNGLSTYGYGTTTDPLEIYIVESGYGYNSSGCTKGYVTSDSGSYDYLXATFNMAA	161
Oy	127	SIICATATFYVYVSVRRNHSSSGSVNTANFNAWAQOGLTLGTMDOYIVAAVEGYSSGSAS	186
Db	162	SIGATATFTQYVSVRQNKREVGCTVTTSNFNAAMAKLGMNLGTHNYQIVALEGYOSSGSSS	221
Oy	187	ITV 189	
Db	222	ITV 224	
RESULT 7			
ID	XYNI_COCOA	STANDARD;	PRT; 221 AA.
AC	065F2;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Endo-1,4-beta-xylanase I precursor (Ec 3.2.1.8) (Xylanase I)		
DE	(1,4-beta-D-xylan xylanohydrolase 1).		
GN	XYLI		
OS	Cochliobolus carbonum (Bipolaris zeicola).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;		
OC	Pleosporales; Pleosporaceae; Cochliobolus.		
OX	NCBI_Taxid=5017;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-Race 1 / Isolate SB11;		
RX	MEDLINE=94003417; PubMed=8400376;		
RA	Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;		
RT	"Cloning and targeted gene disruption of Xyl1, a beta 1,4-xylanase		
RT	gene from the maize pathogen Cochliobolus carbonum.";		
RL	Mo1. Plant Microbe Interact. 6:467-473 (1993).		
RE	[2]		
RA	PARTIAL SEQUENCE.		
RT	Holden F.R., Walton J.D.;		
RL	"Xylanases from the fungal maize pathogen Cochliobolus carbonum.";		
RT	Physiol. Mol. Plant Pathol. 40:39-47 (1992).		
CC	-1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE		
CC	HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-		
CC	WALLS.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylansidic		
CC	linkages in xyilans.		
CC	-1- PATHWAY: Xylan degradation.		
CC	-1- SUBCELLULAR LOCATION: Secreted.		
CC	-1- PTM: The N-terminus is blocked.		
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl		
CC	hydrolases).		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; L13596; AAA33024.1; -		
DR	HSSP; O43097; IYNA.		
DR	InterPro; IPR008985; Cons1 like lec g1.		
DR	InterPro; IPR001137; Glyco_hydro_11.		
DR	Pfam; PF00457; Glyco_hydro_11; 1.		
DR	PRINTS; PRO0911; GLHYDRLASE11.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KM	Xylan degradation; Hydrolase; Glycosidase; Signal.		
FT	SIGNAL	1	30
FT	CHAIN	31	221
FT	ACT_SITE	115	115
FT	ACT_SITE	206	206
FT	CONFLICT	81	81
FT	W -> I (IN REF. 2).		

FT	CONFLICT	107	107	G -> A (IN REF. 2)
FT	CONFLICT	131	131	S -> M (IN REF. 2)
SO	SEQUENCE	221 AA;	23728 MW;	59DBD893F5CB05C CRC64;
	Query Match		62.2%;	Score 650.5; DB 1; Length 221;
	Best Local Similarity		62.1%;	Pred. No. 3.8e-46;
	Matches 118;	Conservative	26;	Mismatches 45; Indels 1; Gaps 1
Qy	1	QTTQPGTGNNGYFYSYNDHGHGVTYTNNGGGCFSTYVMSNSGNFVGGKMGOGCTKNKYI	60	
Db	31	QNTPNBEGHNCFCFMSWSDGARATYTNAGGSGYSWMSGGLVGGKMGWNGTA-RTI	89	
Qy	61	NFSGSYNPNGNSYLVYVGMSENPLEEYIVNFPNTSPGTATLGEVTSIDGSGVYDIYRT	120	
Db	90	TVSGTITNNKNSYLVAYGTGNPLVEYIVNFPNTSPGTATLGEVTSIDGSGVYDIYRT	149	
Qy	121	QRVNPSIIIGATPTQVYSVERNRHSSGGSVNTANHPMAAQGLTGTMDYQIVAVEGYF	180	
Db	150	TRFNQPSIDGRTFQOYMSVSRQNRKSSGVSVMKTHFPAMASKGNLQGHYYQIVATEGYF	209	
Qy	181	SSGSAISITVS	190	
Db	210	STGNAGITVN	219	
RESULT 8				
XXNA	THELA	STANDARD;	PRT;	225 AA.
ID	XXNA	THELA		
AC	043037;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	End-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan xylanohydrolase).			
GN	XXNA.			
OS	Thermomyces lanuginosus (Humicola lanuginosa).			
OC	Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.			
OX	NCBI_TaxID=5541;			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=DSM 5826 / Tsiklinsky;			
RC	MEDLINE=97033440; PubMed=8879171;			
RX	Schlicher A., Holzmann K., Hayn W., Steiner W., Schnab H.;			
RA	"Cloning and characterization of the gene for the thermostable			
RT	xylanase XXNA from Thermomyces lanuginosus.";			
RL	J. Biotechnol. 49:211-218 (1996).			
RJ	[2]			
RP	X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).			
RC	STRAIN=DSM 5826 / Tsiklinsky;			
RX	MEDLINE=98426042; PubMed=9753433;			
RA	Gruber K., Kintschchar G., Hayn W., Schlacher A., Steiner W.,			
RA	Kracy C.;			
RT	"Thermophilic xylanase from Thermomyces lanuginosus: high-resolution			
RL	X-ray structure and modeling studies.";			
RL	Biochemistry 37:13475-13485 (1998)			
CC	- FUNCTION: THERMOSTABLE XILANASE.			
CC	- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	- PATHWAY: xylan degradation.			
CC	- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl			
CC	hydrolases).			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/ ,			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U35436; AA94633.1; -.			
DR	PDB; 1YNA; 12-FEB-97.			
RR	InterPro; IPR008985; COMA like lec g1.			

InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYCOLASEL1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;
 KW Pyrrolidone carboxylic acid.

FT SIGNAL 1 31
 FT CHAIN 32 225 ENO-1,4-BETA-XYLANASE.
 FT ACT_SITE 117 117 NUCLEOPHILE.
 FT ACT_SITE 209 209 PROTON DONOR.
 FT MOD_RES 32 32 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 141 185

FT STRAND 33 33
 FT TURN 37 41
 FT TURN 42 43
 FT STRAND 44 50
 FT STRAND 56 60
 FT TURN 63 64
 FT STRAND 65 70
 FT STRAND 75 82
 FT STRAND 90 100
 FT STRAND 103 112
 FT TURN 113 115
 FT STRAND 116 124
 FT TURN 129 132
 FT STRAND 134 141
 FT TURN 142 143
 FT STRAND 144 158
 FT TURN 159 160
 FT STRAND 161 172
 FT STRAND 179 182
 FT HELIX 183 192
 FT TURN 193 194
 FT TURN 200 211
 FT STRAND 214 223
 SQ SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 60.8%; Score 635.5; DB 1; Length 225;
 Best Local Similarity 60.2%; Pred. No. 6.4e-45;
 Matches 115; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

QY 1 OTTPGNGYNNGVYGVYVWNGHGGVYTYTNGPGGPGSVWNSGNGFVGKMGQGTGKXKVI 60
 DB 32 CTTPNSRGWHDGYYSWMSDGAQATYTNLEGGTYEISKWDGGLVVGKMGGLNARAI 91
 QY 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
 DB 92 HFEVYQNGNSYLAAYGWTNRNPLVEYIYVENFGTYDPPSSGATDLGTVCDGSIVRLGKT 151
 QY 121 QRVNPGSLTGATFYQYWSVRNRNRSSGSVNTANHFMAAQQGLTL-GTYDYQIVAVEGY 179
 DB 152 TRVAPPSIDGTQTFDQYWSVRQDKRTSGTVQTCGFAMAPARGLVNGDHYQIVAVEGY 211
 QY 180 FSSGSASTVS 190
 DB 212 FSSGVARITVA 222

RESULT 9
 XYNB_HUMIN STANDARD; PRT; 227 AA.
 ID XYNB_HUMIN
 AC P55314; O12625;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 GN XYL1.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94247364; PubMed=8190078;
 RA Dalboe H, Hansen H.P.H.;
 RT "A novel method for efficient expression cloning of fungal enzyme
 genes.";
 RL Mol. Gen. Genet. 243:253-260(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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 CC or send an email to license@ebi.ac.uk).

DR EMBL; X76047; CAA53632.1; -
 DR PIR; S43919; S43919.
 DR HSSP; O43097; 1YNA.
 DR InterPro: IPR008985; Cons. like lec 91.
 DR InterPro: IPR01137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYCOLASEL1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 227 ENO-1,4-BETA-XYLANASE 1.
 FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 227 AA; 25601 MW; 5CFEADCFEADALF CRC64;

Query Match 58.8%; Score 614.5; DB 1; Length 227;
 Best Local Similarity 58.8%; Pred. No. 3.3e-43;
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGFYFSYNDHGGVYTYTNGPGGPGSVWNSGNGFVGKMGQGTGKXKVINFSYSN 67
 DB 44 GHNHYFYFSWMSDGGQVQYTNLEGSRYQVWRNRTGNGVSKGNPGL-GRTINYGGRN 102
 QY 68 PNGNSYLSYVWGSRNPLIEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRTQVNOP 127
 DB 103 PGNNGYLAAYGWTNRNPLVEYIYVENFGTYNPGTATKLGVTSDGSVYDIYRTQVNOP 162
 QY 128 IIGTATFYQYWSVRNRNRSSGSVNTANHFMAAQQGLTLGTYDYQIVAVEGYFSSGASI 187
 DB 163 IDGTFTQCYWSIRNRKKEVGSVNMQNHFMMAQQGLGTHYQVVAITEGYQSSGESDI 222
 QY 188 TV 189
 DB 223 YV 224

RESULT 10
 XYNB_STRLI STANDARD; PRT; 335 AA.
 ID XYNB_STRLI
 AC P26515;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
 GN XLNB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomyces; Streptomyces; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.

RC STRAIN=66 / 1326;
 RA MEDLINE=92077439; PubMed=1743521;
 RT "Sequences of three genes specifying xylanases in Streptomyces lividans";
 RL Gene 107:75-82(1991).
 RN [2]
 RP REVISIONS TO 29-32 AND 252-307.
 RX STRAIN=66 / 1326; PubMed=7533741;
 RA Shareck F., Biely P., Morosoli R., Kluepfel D.;
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans reveals genes encoding acetyl xylan esterase and the RNA component of ribonuclease P";
 RL Gene 153:105-109(1995).
 RN [3]
 RP REVISION TO 225.
 RA Shareck F.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major component of plant cell-walls. XLN4 and XLN5 seem to act sequentially on the substrate to yield xylobiose and xylose as carbon sources.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl hydrolases).
 CC -----
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 CC -----
 DR EMBL; M04552; AAC06114.2; -;
 DR HSP; P09850; IKNB.
 DR InterPro; IPR001919; Bac celose-bind.
 DR InterPro; IPR008965; Cellul bind.
 DR InterPro; IPR008985; Cons like lec_g1.
 DR InterPro; IPR001137; Glyco hydro_11.
 DR Pfam; PF00457; Glyco hydro_11; 1.
 DR PRINTS; PR00911; GHYDRLASE11.
 DR SMART; SM00637; CBD_II; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 41
 FT CHAIN 42 335 ENDO-1,4-BETA-XYLANASE B.
 FT DOMAIN 42 230 CATALYTIC.
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 250 335 XILAN-BINDING (POTENTIAL).
 FT ACT_SITE 128 128 NUCLEOPHILS (BY SIMILARITY).
 FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8F0CF CRC64;
 Query March 56.8%; Score 594; DB 1; Length 335;
 Best local similarity 55.1%; Pred. No. 2,4e-41; Indels 16; Gaps 5;
 Matches 109; Conservative 32; Mismatches 41;
 5 PGT-----GYNNGYFYSYNDGHHGVYTYNGPGGQPSVNMNSGNGFVGKQW 52
 36 PGTAAQADVVTNNEGNNNGYGFWDSDGYSMMNGSGOYSTWRNNGNFVAGKWA 95
 53 PGTAKKINSGSYNPNKNSYLSYGSWRPLLEYVVENFGTNPSTGATKXGEVTS 112
 96 NGGR-RIVQYSGSNPFGNATLALYGMTSNPLVEYIVDWMGTRP-TGEYK-GYVTS 152
 113 SYVDIYTORVNDPSIGTATFYGVMSVRNRHSSGSVNTANFNMAAQGLTIGTD-Y 171

Db 153 GTYDIYKTRVKNPSVEGRTTDPQYWSVRQSKRTGGTITGNHFDAPARACNPLGNPSY 212
 QY 172 QIVAVEGYPSGSGASITV 189
 Db 213 MIMATEGYSSGSSSINV 230
 RESULT 11
 ID XYNB CELFI STANDARD; PRT; 644 AA.
 AC P54865;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
 GN XYNB.
 OS Cellulomonas fimi.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Cellulomonadaceae; Cellulomonas.
 OX NCBI_TaxID-1708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=221;
 RX MEDLINE=9422415; PubMed=8170399;
 RA Millward-Sadler S.J., Poole D.M., Hemmisset B., Hazlewood G.P., Clarke J.H., Gilbert H.J.;
 RT "Evidence for a general role for high-affinity non-catalytic cellulose binding domains in microbial plant cell wall hydrolases";
 RL Mol. Microbiol. 11:375-382(1994).
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable activity against polysaccharides other than xylan. Hydrolyzes glucosidic bonds with retention of anomeric configuration.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl hydrolases).
 CC -----
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 CC -----
 DR EMBL; X76729; CA54145.1; -;
 DR PIR; I40712; I40712.
 DR PDB; 1ESB; 25-MAY-01.
 DR PDB; 1ESC; 25-MAY-01.
 DR PDB; 1HEH; 10-MAY-01.
 DR PDB; 1HEH; 10-MAY-01.
 DR PDB; 1XED; 21-JUL-99.
 DR PDB; 2XED; 21-JUL-99.
 DR InterPro; IPR001919; Bac celose-bind.
 DR InterPro; IPR008965; Cellul bind.
 DR InterPro; IPR008985; Cons like lec_g1.
 DR InterPro; IPR001137; Glyco hydro_11.
 DR InterPro; IPR002509; Polysac_deacet.
 DR Pfam; PF00553; CBM_2; 2.
 DR Pfam; PF00457; Glyco hydro_11; 1.
 DR Pfam; PF01522; Polysac_deacet; 1.
 DR SMART; SM00637; CBD_II; 2.
 DR SMART; SM00911; GHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat;
 KM 3D-structure.
 FT SIGNAL 1 43
 FT CHAIN 44 644 ENDO-1,4-BETA-XYLANASE D.
 FT DOMAIN 44 230 CATALYTIC.
 FT DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 246 644 2 X 98 AA APPROXIMATE CBD-LIKE REPEATS.

FT REPEAT 246 333 1.
 FT REPEAT 557 644 2.
 FT DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).
 FT DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 231 238 POLY-GLY.
 FT DOMAIN 241 245 POLY-GLY.
 FT DOMAIN 548 558 POLY-GLY.
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 644 AA; 66581 MW; 56B045CC6E0E1820 CRC64;

Query Match 55.1%; Score 575.5; DB 1; Length 644;
 Best Local Similarity 55.7%; Pred. No. 1.6e-39;
 Matches 103; Conservative 39; Mismatches 38; Indels 5; Gaps 4;

QY 7 TGVNNGYFYGVNDGHHGVYTYNGPGGFSVNSNSGNFVGKGMQPGTKNKYINSGSY 66
 DB 49 TGHHDGFYFSFWIDSPSSVSMDLNSGGIT-RMSNTNFVAGKGMSTGGR-KTVISSGGF 106
 QY 67 NPNGNSYLSVYGMSRNPLEFYIVENFGYTNPSTGATKLGCVTSDSGYDIYRTQVNP 126
 DB 107 NPSRNAYLTLYGWTQSPLEVEYIYDSWGTFRPT--GTFMGTVTSDGTYDIYRTQVNP 164
 QY 127 SIIC-TATFYQYNSVRNRHSSGCVNTANFNMAAQGLTLGMDYQIVAVEGFSSGA 185
 DB 165 SIEDSSIFYQYNSVFRQQRKTGTTISGNHFDAMASKXNKLGRHNYMTATEBGYQSSGS 224
 QY 186 SITVS 190
 DB 225 SITVS 229

RESULT 12
 XYN2_MAGGR STANDARD; PRT; 233 AA.

AC P55335; 001171;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
 DE (1,4-beta-D-xylan xylanohydrolase 22).
 GN XYN2.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
 OC Sordariomycetes; incertae sedis; Magnaportheaceae; Magnaporthe.
 OC NCBI_TaxID=148305;
 RX MEDLINE=96172742; PubMed=8589407;
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;
 RT "Purification, cloning and characterization of two xylanases from
 Magnaporthe grisea, the rice blast fungus";
 RL Mol. Plant Microbe Interact. 8:506-514(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 hydrolases).

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DR EMBL; L37529; AAC41683.1; -
 DR HSSP; O43097; IYNA.
 DR InterPro; IPR008985; CONA like lec g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 39
 FT CHAIN 40 233
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 233 AA; 25491 MW; 400963835F581F98 CRC64;

Query Match 54.7%; Score 571.5; DB 1; Length 233;
 Best Local Similarity 51.8%; Pred. No. 1.1e-39;
 Matches 99; Conservative 35; Mismatches 54; Indels 3; Gaps 2;

QY 1 QTIQPTGVNNGYFYGVNDGHHGVYTYNGPGGFSVNSNSGNFVGKGMQPGTKNKYI 60
 DB 40 QSTPSTRHNGYGYYSWMTDASPVOYQNGKSGSYSVOMSGGNFVGKGMFG-CSKSI 98
 QY 61 NPSGSYNP--NGNSLSVYGMSRNPLEFYIVENFGYTNPSTGATKLGCVTSDSGYDIY 118
 DB 99 TYSGFENSVNNGNALCTYGWTQNPVLEVEYILENVEYENPENSQSRGTLOAGGTYTLH 158
 QY 119 RTQRYNQPSTIGTATFYQYNSVRNRHSSGCVNTANFNMAAQGLTLGMDYQIVAVEG 178
 DB 159 ESTRYNQPSIEGRTFFQYMAIRQQRKNSGTVNTGFFQAMERAGMGNHNYMTATEG 218
 QY 179 YPSSGSASITV 189
 DB 219 YRSAGNSINIV 229

RESULT 13
 XYN1_SCHCO STANDARD; PRT; 197 AA.

AC P35809;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
 xylanohydrolase A).
 GN XYN1.
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OC NCBI_TaxID=5334;
 RX MEDLINE=94063044; PubMed=8243636;
 RA Oku T., Roy C., Watson D.C., Wakarchuk W., Yaguchi M.,
 RA Juresek L., Paice M.G.;
 RT "Amino acid sequence and thermostability of xylanase A from
 Schizophyllum commune";
 RT FEBS Lett. 334:296-300(1993).
 RN (3)
 RP STRAIN=ATCC 38548 / Delmar;
 RC STRAIN=ATCC 38548 / Delmar;
 RX MEDLINE=94155888; PubMed=7906649;
 RA Bray M.R., Clarke A.J.;
 RT "Identification of a glutamate residue at the active site of xylanase
 A from Schizophyllum commune";
 RT Eur. J. Biochem. 219:821-827(1994).
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
 CC xylanase has a very broad pH activity.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 linkages in xylans.

```

CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
DR PIR: A44597; A44597.
DR HSSP: O43097; IYNA.
DR InterPro: IPR008985; Cons. like lec. g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase.
FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
FT DISULFID 111 160
SQ SEQUENCE 197 AA; 20978 MW; 42C8074B67C1FB83 CRC64;

Query Match 54.1%; Score 565.5; DB 1; Length 197;
Best Local Similarity 55.0%; Pred. No. 2.7e-39;
Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

QY 7 TGVNNGYFYSYWMDHGVVTYNTGPGQGFVSNMS-NGNPVYGGKQMPGTRKNKYNISGS 65
DB 7 TGTGCGYYSWMTDAGADATYQNNGGSGYTLTWSGNNGLVGGKMPGASRSISYSGT 66
QY 66 YNPNGNSYLSVYSGSRNPLIEYIVENFGTYNPSTGATKLGEVTSDDGSVDYDTRQVNO 125
DB 67 YQPNGNSYLSVYSGSRNPLIEYIVENFGTYNPSTGATKLGEVTSDDGSVDYDTRQVNO 126
QY 126 PSITGATFYQYMSYRNRHRS-----SGSVTANHFPMNAOQGLTLGT-MDYQVAVEGY 179
DB 127 PSIDGTQFEQFQWVRPKKAPGSGISQTVDOVCFPMKGLGNLGSSEHNYQIVATEGY 186
QY 180 FSSGSASITVS 190
DB 187 QSSGTATITVT 197

RESULT 14
XVNC STRLI STANDARD; PRT; 240 AA.
AC P66220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XINC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Sharck F., Roy C., Yasuchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RT lividans."
RL Gene 107:75-82(1991).
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
CC component of plant cell-walls.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL: M64553; AAA26836.1; -.
DR EMBL: A25307; CA01768.1; -.
DR PIR: J05091; J05091.
DR HSSP: P09850; IYNA.
DR InterPro: IPR008985; Cons. like lec. g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR InterPro: IPR006311; Tat.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR TIGRFAMs: TIGR01409; Tat_signal_seg; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 49
FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 50.4%; Score 527; DB 1; Length 240;
Best Local Similarity 53.1%; Pred. No. 4.6e-36;
Matches 102; Conservative 30; Mismatches 50; Indels 10; Gaps 6;

QY 2 TTOPGVNNGYFYSYWMDHGVVTYNTGPGQGFVSNMSNGNPVYGGKQMPGTRKNKYN 61
DB 55 TTOPGVNNGYFYSYWMDHGVVTYNTGPGQGFVSNMSNGNPVYGGKQMPGTRKNKYN 61
QY 62 FSSGSYNPNGNSYLSVYSGSRNPLIEYIVENFGTYNPSTGATKLGEVTSDDGSVDYDTRQ 121
DB 110 YNGYFNPVNGYGCGLYGMTSNPLVEYIYIDMNGSYR-IGTYK-GTVSSDGGTYDIYQTT 167
QY 122 RVNQPSTIGTATFYQYMSYRNRHRS--VNTANHFPMNAOQGLTLGMD-YQVAVEGY 178
DB 168 RVNAPVEGTGTFQOQWVSYSKVSQSGITITGNHFPAMARAGNMQFRYYMTMATEG 227
QY 179 YFSSGSASITVS 190
DB 228 YOSSGSSTITVS 239

RESULT 15
XVNA BACST STANDARD; PRT; 210 AA.
AC P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-UTL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XVNA.
OS Bacillus steareothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RT "Nucleotide sequence analysis of an endo-xylanase gene (xyna) from
RT Bacillus steareothermophilus."
RL J. Microbiol. Biotechnol. 5:117-124(1995).
RN [2]
RP REVISIONS.
RC STRAIN=NO. 236;
RA Cho S., Choi Y.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.

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CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U15985; AAB72117.1; -.
CC HSSP; P09850; 1XNB.
CC InterPro; IPR008985; ConA_like lec.gl.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F12_1; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC SIGNAL
CC FT CHAIN 1 19 POTENTIAL.
CC FT ACT_SITE 20 210 ENDO-1,4-BETA-XYLANASE A.
CC FT ACT_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT_SITE 197 197 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;
SQ

Query Match 50.3%; Score 525.5; DB 1; Length 210;
Best Local Similarity 54.1%; Pred. No. 5,3e-36;
Matches 98; Conservative 31; Mismatches 45; Indels 7; Gaps 5;

QY 14 FYSYWNDDHGCVTYTNGPGGQFSYVNSNSGNFVGKGMQPGTKKRVINF-SGSYNPNQNS 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 31 YWQYWTDDGGWVNAVNPGGNYSVTWQNTGNFVVGKGMVTSPPRVINYNAGIWPSPGNG 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 YLSYVGSRNPLIEYIVENFGTNPSTGATKLGVTSDGSVYDIYRTQKRNQPSIIQTA 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 91 YLTLYGWRNALIYYVVDSSWGYTRP-TGNYK-GTVNSDGTIDYITTMRYNAPSIDGTQ 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 133 TFQYWSYVRNRNRSSG--SYNTANHFNNAAQGLTIG-TMDYQIVAVEGYFSSGSASIT 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 TFQFWSYVRQSKRTGNSVSIITFNNHYNAWRSKGMNIGSSMAYQVLATGEGYQSSGRSNVT 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 189 V 189
Db 209 V 209

```

Search completed: June 30, 2004, 19:40:08
 Job time : 8.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 / Search time 33 Seconds

(without alignments)
1816.620 Million cell updates/sec

Title: US-09-856-025B-16

Perfect score: 1045
Sequence: 1 QTIQPTGTGNNGYFSSYWN.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: SPREMBL_25:*
2: sp_archaea:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvtnus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1045	100.0	223	3	002244
2	1033	98.9	223	3	099015
3	937	89.7	223	3	072803
4	907	86.8	223	3	081074
5	876	83.8	223	3	090V99
6	765.5	73.3	241	3	012580
7	757.5	72.5	293	3	0871B8
8	721.5	69.0	261	3	08U1V6
9	705.5	67.5	219	3	012579
10	701.5	67.1	232	3	09HFA4
11	696.5	66.7	290	3	09HEZ0
12	696.5	66.7	290	3	09HEZ0
13	686.5	65.7	295	3	09C1R2
14	680.5	65.1	227	3	000263
15	678.5	64.9	227	3	09UVZ3
16	665.5	63.7	225	3	08TG22

17	656.5	62.8	230	3	08U1V5	08U1V5 chaetomium
18	656	62.8	223	3	09U0Q2	09U0Q2 penicillium
19	647.5	62.0	221	3	09HFH0	09HFH0 penicillium
20	635.5	60.8	231	3	013447	013447 cochlidiobolus
21	632.5	60.5	346	2	08VUT4	08VUT4 pseudomonas
22	629.5	60.2	221	3	087037	087037 aspergillus
23	628.5	60.1	231	3	000350	000350 cochlidiobolus
24	623.5	59.7	194	3	081536	081536 pseudomonas
25	616.5	59.0	231	3	072A57	072A57 gibberella
26	615.5	58.9	227	3	09HGB1	09HGB1 humicola
27	613.5	58.7	283	3	096UV7	096UV7 lentinula
28	609.5	58.3	335	2	008346	008346 streptomyces
29	609.5	58.3	335	2	09RMM4	09RMM4 streptomyces
30	608.5	58.2	338	2	09RQB8	09RQB8 pseudomonas
31	607.5	58.1	338	2	056265	056265 thermomonas
32	606.5	58.0	231	3	09C1R1	09C1R1 fusarium ox
33	598	57.2	228	2	059962	059962 streptomyces
34	596.5	57.1	344	2	08GMV7	08GMV7 nomomuraea
35	596	57.0	216	3	074716	074716 claviceps p
36	591.5	56.6	329	2	09RMB9	09RMB9 streptomyces
37	591	56.6	335	16	09RKN6	09RKN6 streptomyces
38	567	54.3	191	2	09EW89	09EW89 pseudomonas
39	536.5	51.3	661	2	059674	059674 pseudomonas
40	532	50.9	352	2	084DD2	084DD2 uncultured
41	530.5	50.8	241	16	09R172	09R172 streptomyces
42	528.5	50.6	361	2	052375	052375 caldicellul
43	526.5	50.4	656	2	059300	059300 cellvibrio
44	525	50.2	240	2	056013	056013 streptomyces
45	524.5	50.2	210	16	09KEF3	09KEF3 bacillus ha

ALIGNMENTS

RESULT 1
ID 002244 PRELIMINARY: PRT; 223 AA.
AC 002244:
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endoxylanase II (BC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XLN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94088442; PubMed=8264524;
RA Saaralahti R., Paloheimo M., Fagerstrom R., Suominen P.L.,
RA Nevalainen K.M.;
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei
RT endoxylanase II (pI 9) gene xln2".
RL Mol. Gen. Genet. 241:497-503 (1993).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC EMBL: S67387; AAB29346.1; -;
CC PIR: S39883; S39883.
DR HSSP: P36217; 1XVO.
DR GO: GO:004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; ConA like lec.gl.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosylase; Hydrolyase; Xylan degradation.
KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22F9 CRC64;

Query Match 100.0%; Score 1045; DB 3; Length 223;
 Best Local Similarity 100.0%; Pred. No. 2.6e-70;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 60
 DB 34 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 93
 QY 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 120
 DB 94 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 153
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

AC Q99015;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYN2.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=QM 6a;
 RX MEDLINE=97076932; PubMed=8975597;
 RA la Grange D.C., Pretorius I.S., van Zyl W.H.;
 RT "Expression of a trichoderma reesei beta-xylanase gene (XYN2) in
 RT Saccharomyces cerevisiae";
 RL Appl. Environ. Microbiol. 62:1036-1044(1996).
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: U24191; AAB50278.1; -.
 DR HSSP; P36217; IXXO.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; ConA like lec gl.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR0911; GLHYDRLASE11.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F1_2; 1.
 KW Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT SIGNAL 1
 FT CHAIN 34
 FT 1 223 POTENTIAL.
 FT 223 BETA-XYLANASE.
 SQ SEQUENCE 223 AA; 23981 MW; F696545DAC0B54 CRC64;

Query Match 98.9%; Score 1033; DB 3; Length 223;
 Best Local Similarity 98.9%; Pred. No. 2.1e-69;
 Matches 188; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 60
 DB 34 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 93
 QY 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 120

DB 94 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 153
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 3

Q72803 PRELIMINARY; PRT; 223 AA.

AC Q72803;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
 OS Trichoderma viride.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YNCC0183;
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,
 RA Yang Z.W.;
 RT "Cloning and characterization of endo-1,4-beta-xylanase from
 RT Trichoderma viride (YNUCC0183)."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY320048; AAP81925.1; -.
 KW Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4E76FA03CAE CRC64;

Query Match 89.7%; Score 937; DB 3; Length 223;
 Best Local Similarity 87.4%; Pred. No. 2.9e-62;
 Matches 166; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 60
 DB 34 QTIQPGTGNNGYFYSYVNDGSGVTYTNPGGQFSYVMSNSGNFVGKGMQGTGKXVI 93
 QY 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 120
 DB 94 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATRLGCVTSDSGSVDIYRT 153
 QY 121 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 180
 DB 154 QRVNQPSTIIIGTATFYQYVSVRRNRRSSGSVNTANHFNAQAQGLTLGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.

AC Q8J0T4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Xylanase.
 OS Trichoderma sp. SY.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=215577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SY;
 RA Min S.Y., Kim B.G., Ahn J.-H.;
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from

RT Fungus Trichoderma Strain SY.
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY156910; AA018423.1.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; Cons like lec.g1.
 DR InterPro: IPR001137; Glyco_hydro.11.
 DR Pfam: PF00457; Glyco_hydro.11.
 DR PRINTS: PR00311; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1, 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2, 1.
 DR SEQUENCE 220 AA; 23814 MW; 10EB87D5168B05EF CRC64;
 Query Match 86.8%; Score 907; DB 3; Length 220;
 Best Local Similarity 84.7%; Pred. No. 4.9e-60;
 Matches 161; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
 QY 1 QTIQPTGYNNGYFYVWMDHGAVTYTNGPGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
 DB 31 CVIAPGTGFNNGYYSYWNDSHGAVTYTNGAGSFSVMNANGNFVGKMGKMPSSSRRTI 90
 QY 61 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 120
 DB 91 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 150
 QY 121 QRVNQPSTIGTATFYQVWSVVRNHRSSGSVNTANHFMAAQQGLTLGTMVQIYAVEGYF 180
 DB 151 QRVNQPSTIGTATFYQVWSVVRNHRSSGSVNTANHFMAAQLGLTLGQIDYQIYAVEGYF 210
 QY 181 SSGSASITVS 190
 DB 211 SSGSANINVS 220
 RESULT 5
 Q9UVF9 PRELIMINARY; PRT; 223 AA.
 ID Q9UVF9
 AC Q9UVF9
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
 OS Trichoderma viride.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furman-Matarasso N., Cohen E., Avni A.;
 RT "Mutations in the Active Site of the E-chylene Inducing Xylanase
 RT Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the
 RT Elicitation Activity."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: AJ012718; CAB60757.1; .
 DR HSBP: P48793; 1XND.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; Cons like lec.g1.
 DR InterPro: IPR001137; Glyco_hydro.11.
 DR Pfam: PF00457; Glyco_hydro.11.
 DR PRINTS: PR00311; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1, 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2, 1.
 DR Glycosidase: Hydrolyase; Signal; Xylan degradation.
 FT SIGNAL 1
 FT CHAIN 34 223
 FT SEQUENCE 223 AA; 24230 MW; FBF812028FB1212A CRC64;

Query Match 83.8%; Score 876; DB 3; Length 223;
 Best Local Similarity 82.1%; Pred. No. 1e-57;
 Matches 156; Conservative 12; Mismatches 22; Indels 0; Gaps 0;
 QY 1 QTIQPTGYNNGYFYVWMDHGAVTYTNGPGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
 DB 34 QTIQPTGYNNGYFYVWMDHGAVTYTNGAGSFSVMNANGNFVGKMGKMPSSSRVI 93
 QY 61 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 120
 DB 94 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 153
 QY 121 QRVNQPSTIGTATFYQVWSVVRNHRSSGSVNTANHFMAAQQGLTLGTMVQIYAVEGYF 180
 DB 154 QRVNQPSTIGTATFYQVWSVVRNHRSSGSVNTANHFMAAQLGLTLGQIDYQIYAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSANINVS 223
 RESULT 6
 Q12580 PRELIMINARY; PRT; 241 AA.
 ID Q12580
 AC Q12580
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-beta-1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN CGXB.
 OS Chaetomium gracile.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
 OX NCBI_TaxID=47794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 RT expression in Aspergillus nidulans."
 RL Curr. Genet. 39:73-80(1995).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: D49851; BAA08650.1; .
 DR FTR: S71473; S71473.
 DR HSBP: P36217; 1XVO.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; Cons like lec.g1.
 DR InterPro: IPR001137; Glyco_hydro.11.
 DR Pfam: PF00457; Glyco_hydro.11.
 DR PRINTS: PR00311; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1, 1.
 DR Glycosidase: Hydrolyase; Xylan degradation.
 KW SEQUENCE 241 AA; 25564 MW; DCD4B012272F77F CRC64;
 Query Match 73.3%; Score 765.5; DB 3; Length 241;
 Best Local Similarity 73.8%; Pred. No. 1.9e-49;
 Matches 135; Conservative 21; Mismatches 26; Indels 1; Gaps 1;
 QY 7 TGVNNGYFYVWMDHGAVTYTNGPGQFVSVMNSGNTFVGKMGQPGTKNKVINFGSY 66
 DB 38 TGVNNGYFYVWMDHGAVTYTNGAGSFSVMNANGNFVGKMGKMPSSSRVI 96
 QY 67 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 126
 DB 97 NFGSYNPNNGNSYLSYGVGSKNPLIEYIVENFGTYNPSGTATKLGAVTSDGSVYDIYRT 156
 QY 127 SIIGTATFYQVWSVVRNHRSSGSVNTANHFMAAQQGLTLGTMVQIYAVEGYFSSGSAS 186

Db 157 SIECTSTFYQFQWVQKRGSGSVNMAHFNMAAAGLQIGTHDYQIVATEGYSSGSAT 216
 QY 187 ITV 189
 Db 217 VNV 219

RESULT 7

ID Q871E8 PRELIMINARY; PRT; 293 AA.
 AC Q871E8;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Probable endo-1, 4-beta-xylanase B.
 GN B6c12.010.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxId=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hohnsels J., Brandt P., Fartmann B., Holland R.,
 RA Nakamura G., Kewes H.W., Mannhaupt G.,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BX294027; CAD71059.1; .
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR00254; CBD_fungal.
 DR InterPro: IPR008985; ConA_like lec gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00724; CBM_1; 1.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fcbd; 1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR GlycoSite; Hydrolase; Xylan degradation.
 KW SEQUENCE 293 AA; 30776 MW; D67AB1CE65930F26 CRC64;

Query Match 72.5%; Score 757.5; DB 3; Length 293;
 Best Local Similarity 72.1%; Pred. No. 9.2e-49;
 Matches 132; Conservative 25; Mismatches 25; Indels 1; Gaps 1;

QY 7 TGINNGYFYQWVNDHGCVYTNPGGQFQSVNNSNGNFVQKMGQGTCKRYINFGSY 66
 Db 42 TGINNGYFYQWVNDHGCVYTNPGGQFQSVNNSNGNFVQKMGQGTCKRYINFGSY 100
 QY 67 NPNNSYLYVYGSRNPLIEYIVENFGYVSTGATKLEVTSDGSVDYITQRYNQP 126
 Db 101 SPNNSYLYVYGSRNPLIEYIVENFGYVSTGATKLEVTSDGSVDYITQRYNQP 160
 QY 127 SIIGTATFYQWVSRNRHSSGSVNTANHFMAAQQGLTIGTMDYQIVAVEGFSSGSAS 186
 Db 161 SIDGTATFYQWVSRNRHSSGSVNTANHFMAAQQGLTIGTMDYQIVAVEGFSSGSST 220
 QY 187 ITV 189
 Db 221 INV 223

RESULT 8
 O871E8 PRELIMINARY; PRT; 261 AA.
 AC O871E8;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endoxylanase 11A precursor.
 GN XYN1A.
 OS Chaetomium thermophilum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
 OX NCBI_TaxId=209285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mantyla A., Palohelmo M., Hakola S., Leskinen S., Vehmanen J.,
 RA Lantto R., Suominen P.,
 RT "Heterologous production of three xylanases from Chaetomium
 thermophilum in Trichoderma reesei";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ508931; CAD48749.1; .
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like lec gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; GLHYDRLASE11.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 KW Signal; Xylan degradation; Hydrolase; Glycosidase.
 FT SIGNAL 1 19
 FT CHAIN 20 261
 FT SEQUENCE 261 AA; 27844 MW; 420D6256334D7707 CRC64;

Query Match 69.0%; Score 721.5; DB 3; Length 261;
 Best Local Similarity 65.8%; Pred. No. 3.8e-46;
 Matches 125; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 1 QTI-QPGYNNNGYFYQWVNDHGCVYTNPGGQFQSVNNSNGNFVQKMGQGTCKRY 59
 Db 27 QTLTSSAGTNGYFYQWVNDHGCVYTNPGGQFQSVNNSNGNFVQKMGQGTCKRY 86
 QY 60 INFSGSYNPNNSYLYVYGSRNPLIEYIVENFGYVSTGATKLEVTSDGSVDYITR 119
 Db 87 INVTADYRPNNSYLYVYGSRNPLIEYIVENFGYVSTGATKLEVTSDGSVDYITR 146
 QY 120 TORVNPSEIIGTATFYQWVSRNRHSSGSVNTANHFMAAQQGLTIGTMDYQIVAVEGY 179
 Db 147 TORVNPSEIIGTATFYQWVSRNRHSSGSVNTANHFMAAQQGLTIGTMDYQIVAVEGY 206
 QY 180 FSSGSASITV 189
 Db 207 YSSGSATVNV 216

RESULT 9
 Q12579 PRELIMINARY; PRT; 219 AA.

ID Q12579;
 AC Q12579;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-beta-1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN CGXA.
 OS Chaetomium gracile.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
 OX NCBI_TaxId=47794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 expression in Aspergillus nidulans";
 RL Curr. Genet. 29:73-80(1995).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.

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CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; D49850; BAB08649.1; -.
DR PIR; S71472; S71472.
DR HSSP; P36217; 1XO.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR InterPro; IPR008985; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2.1.
DR GLYCOSIDASE; Hydrolase; Xylan degradation.
SQ SEQUENCE 219 AA; 23324 MW; 4729299808FD9FBA CRC64;

Query Match 67.5%; Score 705.5; DB 3; Length 219;
Best Local Similarity 68.1%; Pred. No. 4,9e-45;
Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGNNGYFYSYNDGSGVYTYNPGGQSPSVMSNSGNFVGKGMOPGTKNKVINFGS 65
DB GTGNNGYFYSFWTDGGGVYVQNGAGSGSVQWQNGNFVGKGMNPGAA-RTINFGT 94
QY 66 YNPNNGSYLSVGMKSRPLIEYIVENFGTNPSTGATKLGVTSDGSVDYRTQRVNQ 125
DB 95 PSFGNGYLAIVGWTQNPVLEYIVESFGYDPSQSKFGTLTQDDSTYTTAKTRVQ 154
QY 126 PSIIGTATFYQYMSVVRNRRSSGSVNTANFNMAAQGLTGTMDYQIIVAVEGFSSGSA 185
DB 155 PSIGTSTFPDQFWSVRQNHSSGSVNVAHFNMAMAGLKLGSINVOIVATEGQSSGSA 214
QY 186 SITVS 190
DB 215 SITVS 219

RESULT 10
Q9HFA4 PRELIMINARY; PRT; 232 AA.
AC Q9HFA4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYN2G.
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura T., Sakka K., Ohmura K.;
RT "Molecular cloning, overexpression, and purification of major xylanase
RT from Aspergillus oryzae."
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; AB044941; BAB20794.1; -.
DR PIR; JC7577; JC7577.
DR HSSP; P36217; 1XO.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2.1.
DR GLYCOSIDASE; Hydrolase; Xylan degradation.
SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

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Query Match 67.1%; Score 701.5; DB 3; Length 232;
Best Local Similarity 67.8%; Pred. No. 1e-44;
Matches 124; Conservative 25; Mismatches 33; Indels 1; Gaps 1;

QY 7 TGINNGYFYSYNDGSGVYTYNPGGQSPSVMSNSGNFVGKGMOPGTKNKVINFGS 66
DB TGINNGYFYSFWTDGGGVYTYNNGGSGSVQMSVNGNFVGKGMNPGS-SRAITVSSGF 108
QY 67 NPNNGSYLSVGMKSRPLIEYIVENFGTNPSTGATKLGVTSDGSVDYRTQRVNQ 126
DB 109 NSGNGYLAIVGWTQNPVLEYIVESFGYDPSQSKFGTLTQDDSTYTTAKTRVQ 168
QY 127 SIIGTATFYQYMSVVRNRRSSGSVNTANFNMAAQGLTGTMDYQIIVAVEGFSSGSA 186
DB 169 SIIGTATFYQFWSVVRNRRSSGSVNTANFNMAAQGLTGTMDYQIIVAVEGFSSGSA 228
QY 187 ITV 189
DB 229 ITV 231

RESULT 11
Q9HEZ0 PRELIMINARY; PRT; 290 AA.
AC Q9HEZ0;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYNB.
OS Phanerochaete chrysosporium.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Corticiaceae; Phanerochaete.
OX NCBI_TaxID=5306;
RN [1]
RP SEQUENCE FROM N.A.
RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
RT "Molecular characterization and expression analysis of two endo-1,4-B-
RT xylanase genes from Phanerochaete chrysosporium."
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; AF301904; AAG44994.1; -.
DR HSSP; P00725; IAZ6.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR InterPro; IPR00254; CBD_fungal.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00734; CEM 1.
DR Pfam; PF00457; Glyco_hydro_11.
DR PRINTS; PR00911; GLHYDLASE11.
DR PROSITE; PS001821; CBD_fungal; 1.
DR SMART; SM00236; ECB1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2.1.
DR GLYCOSIDASE; Hydrolase; Xylan degradation.
SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;
Best Local Similarity 64.7%; Pred. No. 3.2e-44;
Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 CTIGGTGNNGYFYSYNDGSGVYTYNPGGQSPSVMSNSGNFVGKGMOPGTKNKVI 60
DB 34 CTSTAGTGINNGYFYSFWTDGGGVYTYNNGGSGSVQMSVNGNFVGKGMNPGSAA-0AI 92

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QY 61 NEGSGINPNNSYLSYVGMGRNPLIEYIYENFCTNPSGATKLGCVTSDGSVDYIYRT 120
 Db 93 SFTANYQPNNGNSYLSYVGMSTNPLVEYIILEDFTGNPAVSLTHKGTLLSDGATVDVYEG 152
 QY 121 QRVNOPSIIIGTATFYQVWSVRNRHRSRSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180
 Db 153 TRVNEPSTIGTATFNQVWSIRSKRSRSGVTYTNHNFAMKQLPLGTNTYQIVAVEGYQ 212
 QY 181 SSGSASTVS 190
 Db 213 SSGSSTVTVN 222

RESULT 12

Q9HE9 PRELIMINARY; PRT; 290 AA.
 ID Q9HE9
 AC Q9HE9; 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE ENO-1,4-B-Xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYNB.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_Taxid=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301905; AAC4995.1; -.
 DR HSBP; P00725; IAZ6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; ECD; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Xylan degradation.
 KW SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;

Query Match 66.7%; Score 696.5; DB 3; Length 290;
 Best Local Similarity 64.7%; Pred. No. 3.2e-44;
 Matches 123; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTIQGTGYNNGSYFYVNDGCVTYTNGPGQFVSVMNSGNFVGKGMOPGTNNKVI 60
 Db 34 QSTAGTGTNNGYFSFTDGGSVTYNNGPAGSVTWSNADFAVGKMNPGSA-QAI 92
 QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIYENFCTNPSGATKLGCVTSDGSVDYIYRT 120
 Db 93 SFTANYQPNNGNSYLSYVGMSTNPLVEYIILEDFTGNPAVSLTHKGTLLSDGATVDVYEG 152
 QY 121 QRVNOPSIIIGTATFYQVWSVRNRHRSRSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYF 180
 Db 153 TRVNEPSTIGTATFNQVWSIRSKRSRSGVTYTNHNFAMKQLPLGTNTYQIVAVEGYQ 212
 QY 181 SSGSASTVS 190
 Db 213 SSGSSTVTVN 222

Db 213 SSGSSTVTVN 222

RESULT 13

ID Q9CIR2 PRELIMINARY; PRT; 295 AA.
 AC Q9CIR2
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYL5.
 OS Fusarium oxysporum f. sp. lycopersici.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_Taxid=59765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Hera C., Gomez-Gomez E., Roncero M.;
 RA "Cloning and characterization of two family 11 xylanase genes in
 RT Fusarium oxysporum f. sp. lycopersici."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF246830; AAK27974.1; -.
 DR HSBP; O43097; LYNA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PS00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Xylan degradation.
 KW SEQUENCE 295 AA; 30858 MW; CA441056CDDC104 CRC64;

Query Match 65.7%; Score 686.5; DB 3; Length 295;
 Best Local Similarity 65.2%; Pred. No. 1.8e-43;
 Matches 120; Conservative 26; Mismatches 37; Indels 1; Gaps 1;

QY 7 TGVNNGYVSYVNDGCVTYTNGPGQFVSVMNSGNFVGKGMOPGTNNKVI 66
 Db 40 SGTNNGFYVSWSDGADATYTNNGGYSVEMKGGVNVGKGMSPG-KARTISYECEY 98
 QY 67 NFGNSYLSYVGMGRNPLIEYIYENFCTNPSGATKLGCVTSDGSVDYIYRTQVNOP 126
 Db 99 KENGNSYLSYVGMSTNPLVEYIYVSGFTYVPSGATKKGTVADGSTDYDIFETTRTNAP 158
 QY 127 STIGTATFYQVWSVRNRHRSRSGSVNTANHFNAQAQGLTGTMDYQIVAVEGYSSGSAS 186
 Db 159 SIDGTQTFQVWSVNRHRSRSGSVTGLHFMAMEKAKKLGTHDYQILATEGYSSGSASH 218
 QY 187 ITVS 190
 Db 219 MTVS 222

RESULT 14

ID Q00263 PRELIMINARY; PRT; 227 AA.
 AC Q00263
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-
 DE xylanase).
 GN Ascochyta pisi.
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC mitosporic Pezizomycotina; Ascochyta.

OX NCBI_TaxID=47971;
 RN [1]
 RA SEQUENCE FROM N.A.
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the
 RL phytopathogenic fungus *Ascochyta blight*.";
 CC Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL; Z68891; CA93120.1; -.
 DR HSSP; O43097; 1YNA.
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; Consilike_1ec_91.
 DR InterPro; IPR01137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR KX Glycosidase; Hydrolyase; Signal; Xylan degradation.
 FT SIGNAL 1 19
 SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;
 Query Match 65.1%; Score 680.5; DB 3; Length 227;
 Best Local Similarity 65.3%; Pred. No. 3; 7e-43;
 Matches 126; Conservative 22; Mismatches 40; Indels 5; Gaps 2;
 QY 2 TIGPCT---GYNNGYISYNDGHHGVYTTNGPGGQPSVNMNSNGNFVGKMGQPGTKNYI 57
 DB 34 TARAGTSSOGTHNGCFYSWWTGCAQATYTNAGSGSYVMWKTGKLVGKGMNPGAA- 92
 QY 58 KVINFGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNPSGATKLGVTSDGSVYDI 117
 DB 93 RTIYSGTSPSGNSYLAIVGWTIRNPLIEYIVENFGTYNPSGATKLGVTSDGSVYDI 152
 QY 118 YRTORVNPSP1IGTATFYQYVSVRNRHSSGSVNTANHFNMAAQGLTGTMDYQIVAVE 177
 DB 153 AQTORTNPSP1IDGTOTFOQYWSVRNKRSSGSVNMKTHFDAMAKGMKLGTHNYQIVAVE 212
 QY 178 GYFSSGSASITVS 190
 DB 213 GYFSSGSASITVN 225

RESULT 15
 09UVZ3
 ID 09UVZ3 PRELIMINARY; PRT; 227 AA.
 AC 09UVZ3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 OS XYL1.
 OS Setosphaeria turcica.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Setosphaeria.
 OX NCBI_TaxID=93612;
 RN [1]
 RA SEQUENCE FROM N.A.
 RC STRAIN=H2;
 RA Degefu Y., Paulin L., Petaenen J., Lubbeck P.S.;
 RT "Cloning, sequencing and expression of a xylanase gene from the maize
 RT pathogen *Helminthosporium turcicum* Pass.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AJ238895; CAB52417.1; -.

DR HSSP; O43097; 1YNA.
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; Consilike_1ec_91.
 DR InterPro; IPR01137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR KX Glycosidase; Hydrolyase; Signal; Xylan degradation.
 FT SIGNAL 1 19
 SQ SEQUENCE 227 AA; 24123 MW; BAE6FC075EE5306E CRC64;
 Query Match 64.9%; Score 678.5; DB 3; Length 227;
 Best Local Similarity 64.7%; Pred. No. 5; 2e-43;
 Matches 123; Conservative 23; Mismatches 43; Indels 1; Gaps 1;
 QY 1 OTTQPGTGYNNGYISYNDGHHGVYTTNGPGGQPSVNMNSNGNFVGKMGQPGTKNYI 60
 DB 37 QSTPNCEGTHNGCFYSWWTGCAQATYTNAGSGSYVMWKTGKLVGKGMNPGTA-RTI 95
 QY 61 NFGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNPSGATKLGVTSDGSVYDIYRT 120
 DB 96 TYSQYNPNPNNSYLAIVGWTIRNPLIEYIVENFGTYNPSGATKLGVTSDGSVYDIYRT 155
 QY 121 QVNPSP1IGTATFYQYVSVRNRHSSGSVNTANHFNMAAQGLTGTMDYQIVAVEGYF 180
 DB 156 TTNQPSIDGTOTFOQYWSVRNKRSSGSVNMKTHFDAMAKGMKLGSHYQIVAVEGYF 215
 QY 181 SSGSASITVS 190
 DB 216 SSGSASITVN 225

Search completed: June 30, 2004, 19:43:40
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds
(without alignments)
1130.190 Million cell updates/sec

Title: US-09-856-025b-62
Perfect score: 1056
Sequence: 1 QTIQPTGTGNGYFYSYWMD.....YQIVAVEGFSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	190	2 AAM60743	AAM60743 Xylanase
2	1026	97.2	190	3 AAY99680	AAY99680 T. reesei
3	1026	97.2	190	5 AAE18452	AAE18452 Trichoder
4	1026	97.2	190	7 AAO30259	AAO30259 Trichoder
5	1026	97.2	223	2 AAR47122	AAR47122 PI 9.0 en
6	1026	97.2	223	2 AAM67567	AAM67567 T. reesei
7	1026	97.0	190	3 AAY99735	AAY99735 Mutant T.
8	1023	96.9	190	5 AAE18470	AAE18470 Trichoder
9	1023	96.9	190	5 AAE18495	AAE18495 Trichoder
10	1023	96.9	190	7 AAO30300	AAO30300 Trichoder
11	1022	96.8	190	7 AAO30303	AAO30303 Trichoder
12	1022	96.8	190	7 AAO30301	AAO30301 Trichoder
13	1021	96.7	190	3 AAB48541	AAB48541 Trichoder
14	1021	96.7	190	5 AAB18647	AAB18647 T. reesei
15	1021	96.7	190	7 AAO30304	AAO30304 Trichoder
16	1020	96.6	190	7 AAO30299	AAO30299 Trichoder
17	1019	96.5	190	2 AAM60284	AAM60284 Modified
18	1019	96.5	190	5 AAE18471	AAE18471 Trichoder
19	1019	96.5	190	5 AAO30279	AAO30279 Trichoder
20	1018	96.4	190	5 AAE18496	AAE18496 Trichoder
21	1018	96.4	190	5 AAO30302	AAO30302 Trichoder
22	1017	96.3	190	7 AAO30280	AAO30280 Trichoder
23	1016	96.2	190	3 AAM60744	AAM60744 Xylanase
24	1016	96.2	190	3 AAY99681	AAY99681 T. viride
25	1016	96.2	190	5 AAE18453	AAE18453 Trichoder

26	1015	96.1	190	7 AAO30306	AAO30306 Trichoder
27	1013	95.9	190	7 AAO30307	AAO30307 Trichoder
28	1010	95.6	190	7 AAO30305	AAO30305 Trichoder
29	1010	95.6	223	2 AAM57422	AAM57422 Amino aci
30	1006	95.3	190	7 AAO30293	AAO30293 Trichoder
31	1004	95.1	190	5 AAE18472	AAE18472 Trichoder
32	1004	95.1	190	7 AAO30287	AAO30287 Trichoder
33	1004	95.1	190	7 AAO30294	AAO30294 Trichoder
34	1003	95.0	190	3 AAB48538	AAB48538 Trichoder
35	1003	95.0	190	5 AAO18644	AAO18644 T. viride
36	1002	94.9	190	7 AAO30297	AAO30297 Trichoder
37	1001	94.8	190	5 AAE18476	AAE18476 Trichoder
38	1000	94.7	190	7 AAO30298	AAO30298 Trichoder
39	999	94.6	190	7 AAO30292	AAO30292 Trichoder
40	998	94.5	190	5 AAE18475	AAE18475 Trichoder
41	998	94.5	190	5 AAE18474	AAE18474 Trichoder
42	998	94.5	190	5 AAE18482	AAE18482 Trichoder
43	998	94.5	190	7 AAO30288	AAO30288 Trichoder
44	997	94.4	190	5 AAE18473	AAE18473 Trichoder
45	995	94.2	190	5 AAE18478	AAE18478 Trichoder

ALIGNMENTS

RESULT 1
ID AAM60743 standard; protein; 190 AA.
XX
AC AAM60743;
XX
DT 17-OCT-2003 (revised)
DT 02-SEP-1998 (first entry)
XX
DE Xylanase II of Trichoderma reesei.
XX
KM Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KM thermotolerance; bleach; wood pulp; processing; wheat; maize;
KM digestibility-improving animal feed additive; starch production; mutant.
OS Hypocrea jecorina.
XX
PN EP828002-A2.
XX
PD 11-MAR-1998.
XX
PF 05-SEP-1997; 97BP-00115412.
XX
PR 09-SEP-1996; 96US-00709912.
PA (CANADA) NAT RES COUNCIL CANADA.
PI Sung WL, Yaguchi M, Ishikawa K;
DR WPI; 1998-161100/15.
PT Modified xylanase enzymes - useful for improving wood pulp bleaching,
PT etc.
PS Disclosure; Page 48; 84pp; English.
XX
CC AAM60728-44 represent family 11 xylanases. The specification describes a
CC method for modifying a family 11 xylanase to improve its thermophilicity,
CC alkalophilicity and/or thermotolerance. This method comprises
CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase
CC II or corresponding aligned amino acids of another family 11 xylanase,
CC replacement of one or more amino acid sequences in the N-terminal region
CC with corresponding aligned sequences from another family 11 xylanase to
CC form a chimeric xylanase and/or upstream extension of the N terminus by
CC addition of upto 10 amino acids. The modified xylanases are useful for
CC improving the bleachability of wood pulp by treatment at 55-75 degrees
CC Celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as
CC digestibility-improving animal feed additives. They might also be useful

CC in the processing of wheat or maize for starch production. (Updated on 17
 CC -Oct-2003 to standardise OS field).
 CC
 XX
 SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 2; Length 190;
 Best Local Similarity 96.4%; Pred. No. 5.2e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTTQPTGYNNGFYFSYNDGAGVYTNPGGQFSYVMSNSGNFVGKGMQPGTKXKI 60
 DB 1 OTTQPTGYNNGFYFSYNDGAGVYTNPGGQFSYVMSNSGNFVGKGMQPGTKXKI 60
 QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSYDIYRT 120
 DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSYDIYRT 120
 QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAQOGLTLGTMQYQIVAVEGYF 180
 DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAQOGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 2
 AAY99680
 ID AAY99680 standard; protein; 190 AA.

XX AAY99680;
 AC
 XX 12-SEP-2003 (revised)
 DT 28-SEP-2000 (first entry)
 DE T. reesei xylanase, Xyn II.
 XX Xylanase; animal feed; digestion efficiency; thermostable;
 KM feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.
 XX Hypocrea jecorina.
 OS
 XX WO200029587-A1.
 PN
 XX 25-MAY-2000.
 PD
 XX 16-NOV-1999; 99WO-CA001093.
 PF
 XX 16-NOV-1998; 98US-0108504P.
 PR
 XX (IOGE-) IOGEN CORP.
 PA
 XX Sung WL, Tolan JS;
 PI
 XX WPI, 2000-387799/33.
 DR
 XX N-PSDB; AAA48219.
 DR
 XX Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.
 XX

PS Disclosure; Fig 1; 86pp; English.
 XX Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. The present sequence, xylanase Xyn II, from Trichoderma
 CC reesei, is a xylanase family 11 member. The xylanases of family 11 have
 CC several properties suitable for feed applications, however, they lack the
 CC thermostability required to survive food pelleting. The present sequence
 CC was used to identify non-conserved residues in Family 11 xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.
 CC As a result various thermostable xylanases were identified (AAY9683,
 CC AAY9684, AAY9685, AAY9686, AAY9735 and AAY9736) which would be
 CC useful for animal feeds, especially poultry and swine feed. (Updated on
 CC 12-SEP-2003 to standardise OS field)

SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 3; Length 190;
 Best Local Similarity 96.4%; Pred. No. 5.2e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTTQPTGYNNGFYFSYNDGAGVYTNPGGQFSYVMSNSGNFVGKGMQPGTKXKI 60
 DB 1 OTTQPTGYNNGFYFSYNDGAGVYTNPGGQFSYVMSNSGNFVGKGMQPGTKXKI 60
 QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSYDIYRT 120
 DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSYDIYRT 120
 QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAQOGLTLGTMQYQIVAVEGYF 180
 DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAQOGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 3
 AAE18452
 ID AAE18452 standard; protein; 190 AA.

XX AAE18452;
 AC
 XX 29-AUG-2003 (revised)
 DT 16-MAY-2002 (first entry)
 DE Trichoderma reesei xylanase (TrX), Xyn II.
 XX Trichoderma reesei xylanase (TrX), Xyn II.
 KM Modified xylanase; thermostability; alkalophilicity; industrial process;
 XX pulp manufacture; poultry; swine feed; enzyme; Xyn II.
 OS
 XX Hypocrea jecorina.
 FH
 XX Key Location/Qualifiers
 FT Region 151..162
 FT /note="Helix"
 XX
 XX WO200192487-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 31-MAY-2001; 2001WO-CA000769.
 PF
 XX 31-MAY-2000; 2000US-0213803P.
 PR
 XX (CANA) NAT RES COUNCIL CANADA.
 PA
 XX Sung WL;
 PI
 XX WPI; 2002-171435/22.
 DR
 XX N-PSDB; AAD29410.
 DR
 XX Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 XX

PS Disclosure; Page 80-81; 109pp; English.
 XX The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx), xyn II. (Updated on 29-AUG-2003 to standardise OS field)
 CC XX
 SQ Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 5; Length 190;
 Best Local Similarity 98.4%; Pred. No. 5.2e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYEYFYSYVNDHGQVYTYNPGGQSFVYVMSNSGNFVGKGMQPGTKXKI 60
 DB 1 QTIQPGTGYNNGYEYFYSYVNDHGQVYTYNPGGQSFVYVMSNSGNFVGKGMQPGTKXKI 60
 QY 61 NFSGSYNPNSNSYLSVYGMSSRNPLIEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNSNSYLSVYGMSSRNPLIEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
 QY 121 QRYNOPSIIIGTATFYQVWSVRNRHSSGSVNTACHFNAMAQGLTLGTMQYQIVAVEGYF 180
 DB 121 QRYNOPSIIIGTATFYQVWSVRNRHSSGSVNTAHFNAMAQGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 4

AA030259
 ID AA030259 standard; protein, 190 AA.

AC AA030259;
 XX 23-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)
 DE Trichoderma reesei xylanase II enzyme (Trx).
 XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KM pulp manufacture; poultry feed; swine feed; enzyme.
 XX Hypocrea jecorina.
 OS
 XX WO2003046169-A2.
 PN 05-JUN-2003.
 PD 20-NOV-2002; 2002WO-CA001758.
 PF 21-NOV-2001; 2001US-00990874.
 PR (CANA) NAT RES COUNCIL CANADA.
 XX (CANA) NAT RES COUNCIL CANADA.
 XX Sung WL;
 PI WPI: 2003-513647/48.
 XX Novel modified xylanase useful in industrial process, exhibits improved
 FT thermophilicity, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.
 XX
 PS Claim 1; Fig 2; 105pp; English.
 CC The invention relates to modified xylanase enzyme which exhibits improved
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 97.2%; Score 1026; DB 7; Length 190;
 Best Local Similarity 98.4%; Pred. No. 5.2e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYEYFYSYVNDHGQVYTYNPGGQSFVYVMSNSGNFVGKGMQPGTKXKI 60
 DB 1 QTIQPGTGYNNGYEYFYSYVNDHGQVYTYNPGGQSFVYVMSNSGNFVGKGMQPGTKXKI 60
 QY 61 NFSGSYNPNSNSYLSVYGMSSRNPLIEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNSNSYLSVYGMSSRNPLIEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
 QY 121 QRYNOPSIIIGTATFYQVWSVRNRHSSGSVNTACHFNAMAQGLTLGTMQYQIVAVEGYF 180
 DB 121 QRYNOPSIIIGTATFYQVWSVRNRHSSGSVNTAHFNAMAQGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 5

AAR47122
 ID AAR47122 standard; protein, 223 AA.

AC AAR47122;
 XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-JUN-1994 (first entry)
 DE pI 9.0 endoxylanase.
 XX Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pI 5.5;
 KM pI 9.0; xlnI; xlnII; endoxylanase.
 XX Hypocrea jecorina; OM6a.
 OS
 XX Key Location/Qualifiers
 FH Cleavage-site 19..20
 FT Protein 34..223
 FT Modified-site 71
 FT /label= N-glycosylation_site
 FT /note= "sequence used for prepn. of PCR primer"
 FT Modified-site 94
 FT /label= N-glycosylation_site
 FT Active-site 119
 FT /note= "Glu proposed to be involved with an active site"
 FT Active-site 210
 FT /note= "Glu proposed to be involved with an active site"
 XX
 PN WO9324621-A1.
 XX 09-DEC-1993.
 PD 24-MAY-1993; 93WO-FI000221.
 PF 29-MAY-1992; 92US-00898993.
 PR (ALKO) ALKO OY AB.
 XX (ALKO) ALKO OY AB.
 XX Suominen P, Nevalainen H, Saarelainen R, Paloheimo M, Laitinen T,
 PI Fagerstrom R;
 XX WPI: 1993-405812/50.
 DR N-PSDB; AA054775.
 XX

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed
 PT industry - comprising sequence encoding amino acid sequence of T. reesei
 PT PI 5.5 xylanase.
 XX
 PS Claim 3; Page 77-78; 11pp; English.
 CC The T. reesei xln2 gene coding for the PI 9.0 endoxylanase was isolated
 CC from the wild-type strain QM6. The gene contains one intron of 108
 CC nucleotides and codes for a protein of 223 amino acids in which two
 CC putative N-glycosylation target sites were found. Three different T.
 CC reesei strains were transformed by targeting a construct composed of the
 CC xln2 gene with its own promoter to the endogenous cbh1 locus. Highest
 CC overall prodn. levels for xylanase were obtained using the T. reesei
 CC ALK02721, a genetically engineered strain, as a host. Integration into
 CC the cbh1 locus was not required for enhanced expression under xln2
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)
 CC
 XX Sequence 223 AA;
 SQ
 Query Match 97.2%; Score 1026; DB 2; Length 223;
 Best Local Similarity 98.4%; Pred. No. 6.4e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QTIPTGTGNNNGYFYSYWMDHGVTYTNBGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
 DB 34 QTIPTGTGNNNGYFYSYWMDHGVTYTNBGGQPSVWMSNGNFVGGKGMQPGTKNKVI 93
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 153
 QY 121 QRVNQPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAAQHGLTGTMDYQIYVAEGYF 180
 DB 154 QRVNQPSIIIGTATFYQYMSVRNRHSSGSVNTAHFNMAAQHGLTGTMDYQIYVAEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223
 RESULT 6
 AAM67567
 ID AAM67567 standard; protein; 223 AA.
 XX
 AC AAM67567;
 XX
 DT 17-OCT-2003 (revised)
 DT 02-MAR-1999 (first entry)
 XX
 DE T. reesei xylanase II protein.
 XX
 XX xylanase; xln. reverse transcription; RT-PCR; primer: amplification;
 KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.
 XX
 OS Hypocrea jeorina.
 XX
 XX
 FH Key Location/Qualifiers
 FT 1..19 /note= "primary signal peptide"
 FT Peptide 20..33 /note= "propeptide"
 FT 33..223 /note= "mature xylanase II protein"
 FT Modified-site 71 /note= "N-glycosylated"
 FT Modified-site 94 /note= "N-glycosylated"
 FT Active-site 119 /note= "N-glycosylated"
 FT Active-site 119 /note= "active site residue"
 FT 210 /note= "active site residue"
 FT /note= "active site residue"

XX US5837515-A.
 PN
 XX 17-NOV-1998.
 XX
 PD
 PF 16-SEP-1993; 93US-00121436.
 XX
 PR 16-MAY-1990; 90US-00524306.
 PR 29-MAY-1992; 92US-00869893.
 PR 24-MAY-1993; 93WO-FI000221.
 PR 18-JUN-1993; 93US-00078478.
 XX
 PA (ALKO-) ALKO-VHTIOET OY.
 XX
 PI Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;
 PI Suominen P;
 XX WPI; 1999-023453/02.
 DR N-PSDB; AAV81332.
 XX
 PT Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for
 PT recombinant production of the enzyme, for use in paper and pulp
 PT production.
 PS Claim 3; Fig 3A-B; 52pp; English.
 XX
 CC This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)
 CC which has an isoelectric point (pI) of 9. The coding sequence was
 CC isolated by reverse transcription PCR using the primers AAV81333-V81335
 CC based on amino acid sequence derived from the N-terminal of the purified
 CC protein. The encoded protein contains a 33 amino acid propeptide sequence
 CC with a primary signal peptide cleavage site between residues 19-20. The
 CC mature protein comprises 190 amino acids with a calculated molecular
 CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer
 CC xylan, one of the most abundant carbohydrate components in plants. This
 CC is especially useful in the paper and pulp making industry. (Updated on
 CC 17-OCT-2003 to standardise OS field)
 CC
 XX Sequence 223 AA;
 SQ
 Query Match 97.2%; Score 1026; DB 2; Length 223;
 Best Local Similarity 98.4%; Pred. No. 6.4e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QTIPTGTGNNNGYFYSYWMDHGVTYTNBGGQPSVWMSNGNFVGGKGMQPGTKNKVI 60
 DB 34 QTIPTGTGNNNGYFYSYWMDHGVTYTNBGGQPSVWMSNGNFVGGKGMQPGTKNKVI 93
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 153
 QY 121 QRVNQPSIIIGTATFYQYMSVRNRHSSGSVNTACHFNMAAQHGLTGTMDYQIYVAEGYF 180
 DB 154 QRVNQPSIIIGTATFYQYMSVRNRHSSGSVNTAHFNMAAQHGLTGTMDYQIYVAEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223
 RESULT 7
 AAY99735
 ID AAY99735 standard; protein; 190 AA.
 XX
 AC AAY99735;
 XX
 DT 12-SEP-2003 (revised)
 DT 28-SEP-2000 (first entry)
 XX
 DE Mutant T. reesei xylanase, Ttr-162H.
 XX
 KW xylanase; animal feed; digestion efficiency; thermostable;

KM feed pelleting; enzyme; mutant; mutein; Xyn A; Xyn B; Xyn; Xyn C; Xyn I;
 XN Xyn II.
 XX Hypocrea jecorina.
 OS
 XX WO200029587-A1.
 PN
 XX
 PD 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99WO-CA001093.
 XX
 PR 16-NOV-1998; 98US-0108504P.
 XX
 PA (IOGE-) IOGEN CORP.
 XX
 PI Sung WL, Tojan JS;
 XX
 DR WPI; 2000-387799/33.
 XX
 PT Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.
 PS
 XX Example 3; Page: 86pp; English.
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. Xylanase Xyn II, from *Trichoderma reesei*, is a xylanase
 CC Family 11 member. The xylanases of Family 11 have several properties
 CC suitable for feed applications, however, they lack the thermostability
 CC required to survive food pelleting. The present sequence was used to
 CC identify non-conserved residues in Family 11 xylanases which could be
 CC mutated to introduce desirable properties e.g. thermostability. As a
 CC result various thermostable xylanases were identified (the present
 CC sequence, AA99736, AA99737, AA99738, AA99739 and AA99740) which
 CC would be useful for animal feeds, especially poultry and swine feed.
 CC Note: the present sequence is not shown in the specification but is
 CC derived from the T. reesei wild-type xylanase sequence given in figure 1
 CC (see AA99680). (Updated on 12-Sep-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 190 AA;
 Query Match 97.0%; Score 1024; DB 3; Length 190;
 Best Local Similarity 97.9%; Pred. No. 8e-87;
 Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QTIPTGTGNNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNTFVGKGMQPGTKNKVI 60
 DB 1 QTIPTGTGNNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNTFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSVYSGMSRNPLEYIIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGSYLSVYSGMSRNPLEYIIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQYMSVRRNHRSSGSVNTACHFNMAOHGLTGMTDYOIVAVEGYF 180
 DB 121 QRVNPSIIIGTATFYQYMSVRRNHRSSGSVNTANHFNMAOHGLTGMTDYOIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190
 RESULT 8
 AAE18470
 ID AAE18470 standard; protein; 190 AA.
 XX
 AC AAE18470;
 XX
 DT 16-MAY-2002 (first entry)

XX
 DE Trichoderma reesei xylanase mutant, Trx-75A.
 XX
 KM Modified xylanase; thermostability; alkalophilicity; industrial process;
 KM pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.
 OS
 XX Hypocrea jecorina.
 OS
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Msc-difference 75
 FT /note= "Wild type Ser substituted with Ala"
 XX
 PN WO200192487-A2.
 XX
 XX
 XX 06-DEC-2001.
 PD
 PF 31-MAY-2001; 2001WO-CA000769.
 XX
 PR 31-MAY-2000; 2000US-0213803P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 XX
 DR WPI; 2002-171435/22.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 PS
 XX Claim 42; Page: 109pp; English.
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is *Trichoderma reesei*
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
 CC specification but is derived from wild type xylanase referred as SEQ ID
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
 CC
 XX
 SQ Sequence 190 AA;
 Query Match 96.9%; Score 1023; DB 5; Length 190;
 Best Local Similarity 97.9%; Pred. No. 9.9e-87;
 Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QTIPTGTGNNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNTFVGKGMQPGTKNKVI 60
 DB 1 QTIPTGTGNNNGYFYSYNDGHHGVTYTNPGQGFVSVMNSGNTFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSVYSGMSRNPLEYIIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGSYLSVYSGMSRNPLEYIIVENFGTNPSTGATKLGVTCDGSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQYMSVRRNHRSSGSVNTACHFNMAOHGLTGMTDYOIVAVEGYF 180
 DB 121 QRVNPSIIIGTATFYQYMSVRRNHRSSGSVNTANHFNMAOHGLTGMTDYOIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190
 RESULT 9
 AAE18495
 ID AAE18495 standard; protein; 190 AA.
 XX
 AC AAE18495;

```
XX 16-MAY-2002 (first entry)
DT Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.
XX
DE Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.
XX
OS Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 161 /note= "wild type Gln substituted with Arg"
FT Misc-difference 162 /note= "wild type Gln substituted with His"
FT Misc-difference 165 /note= "wild type Thr substituted with His"
FT Misc-difference 165 /note= "wild type Thr substituted with His"
XX
PN WO200192487-A2.
XX
XX 06-DEC-2001.
XX
XX 31-MAY-2001; 2001WO-CA000769.
XX
XX 31-MAY-2000; 2000US-0213803P.
XX
XX (CANADA) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2002-171435/22.
XX
XX Modified xylanase exhibiting increased thermostability and
XX alkalophilicity useful for industrial processing e.g. for pulp
XX manufacturing.
XX
XX Claim 42; Page; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX useful for bleaching of pulp, processing of precision devices and
XX improved digestibility of poultry and swine feed. Modified xylanase has
XX improved performance at conditions of high temperature and pH and
XX exhibits improved thermostability and/or alkalophilicity in comparison to
XX corresponding native xylanase. The present sequence is Trichoderma reesei
XX xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX specification but is derived from wild type xylanase referred as SEQ ID
XX NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX
XX Sequence 190 AA;
XX
Query Match 96.9%; Score 1023; DB 5; Length 190;
Best Local Similarity 97.9%; Pred. No. 9.9e-87;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGQGFVYVMSNSGNGFVGGKGMQPGTKNKVI 60
Db 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGQGFVYVMSNSGNGFVGGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAFHFNMAHQGLTLGTMDOYIYAVEGYF 180
Db 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAFHFNMAHQGLTLGTMDOYIYAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
```

```
RESULT 10
AAO30300
ID AAO30300 standard; protein; 190 AA.
XX
AC AAO30300;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (S75A).
XX
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
OS Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 75 /note= "wild type Ser substituted with Ala"
FT Misc-difference 75 /note= "wild type Ser substituted with Ala"
FT
XX
PN WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002WO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANADA) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AAO30259)
XX
XX Sequence 190 AA;
XX
Query Match 96.9%; Score 1023; DB 7; Length 190;
Best Local Similarity 97.9%; Pred. No. 9.9e-87;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGQGFVYVMSNSGNGFVGGKGMQPGTKNKVI 60
Db 1 QTIQPGTGYNNGYFYSYVNDGSGVYTNNGPGQGFVYVMSNSGNGFVGGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLSYVGMRSNPLIEYIVENFGTYNPGTATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAFHFNMAHQGLTLGTMDOYIYAVEGYF 180
Db 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAFHFNMAHQGLTLGTMDOYIYAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
```

RESULT 11
AAO30303
ID AAO30303 standard; protein; 190 AA.
XX
XX AAO30303;
AC
XX 03-SEP-2003 (first entry)
DT
XX
XX Trichoderma reesei xylanase II mutant protein (Q161R).
DE
XX
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
XX Hypocrea jecorina.
OS
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 161 /note= "Wild type Gln substituted with Arg"
FT
XX WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002MO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANA) NAT RES COUNCIL CANADA.
XX
XX
PI Sung WL;
DR WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from Trichoderma reesei.
XX
XX
PS Example 1; Page; 105pp; English.
PS
XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AAO30259)
CC
XX
SO Sequence 190 AA;

Query Match 96.8%; Score 1022; DB 7; Length 190;
Best Local Similarity 97.9%; Pred. No. 1.2e-86;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTTQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60
DB 1 OTTQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLGVYGMRSNPLIEYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLGVYGMRSNPLIEYIVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTAFHFNMAAOGGLTGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTAFHFNMAAOGGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190
RESULT 12
AAO30301
ID AAO30301 standard; protein; 190 AA.
XX
XX AAO30301;
AC
XX 03-SEP-2003 (first entry)
DT
XX
XX Trichoderma reesei xylanase II mutant protein (S75G).
DE
XX
XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
XX Hypocrea jecorina.
OS
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"
FT
XX WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002MO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANA) NAT RES COUNCIL CANADA.
XX
XX
PI Sung WL;
DR WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from Trichoderma reesei.
XX
XX
PS Example 1; Page; 105pp; English.
PS
XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AAO30259)
CC
XX
SO Sequence 190 AA;

Query Match 96.8%; Score 1022; DB 7; Length 190;
Best Local Similarity 97.9%; Pred. No. 1.2e-86;
Matches 186; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTTQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60
DB 1 OTTQPGTGYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLGVYGMRSNPLIEYIVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLGVYGMRSNPLIEYIVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTAFHFNMAAOGGLTGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTAFHFNMAAOGGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

RESULT 13
AAB48541
ID AAB48541 standard; protein; 190 AA.
XX
XX AAB48541;
AC
XX 12-SEP-2003 (revised)
DT 05-MAR-2001 (first entry)
XX
XX Trichoderma reesei xyn II xylanase.
DE
XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;
KM bleaching agent.
XX
XX Hypocrea jecorina.
OS
XX WO200068396-A2.
XX
XX 16-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US013172.
XX
XX 12-MAY-1999; 99US-0133714P.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien JM;
XX
XX WPI; 2000-679800/66.
XX
XX Non naturally occurring XA protein with enhanced thermostability.
PT alkalophilicity or thermostability relative to the naturally occurring
PT Bacillus circulans xylanase is used in an agent for bleaching pulp.
XX
XX Disclosure; Fig 16f; 114pp; English.
PS
XX The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 190 AA;

Query Match 96.7%; Score 1021; DB 3; Length 190;
Best Local Similarity 98.4%; Pred. No. 1.5e-86;
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVNMNSGNFVGGKGMQPGTKNKVIN 61
Db 2 TIQGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVNMNSGNFVGGKGMQPGTKNKVIN 61
QY 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKIGEVTCCGSVYDIYRTQ 121
Db 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKIGEVTCCGSVYDIYRTQ 121
QY 122 RVNPSIIIGTATFYQYVSVRRNHRSSGSVNTACHFNMAOGLTLGTMDOQIYAVEGYFS 181
Db 122 RVNPSIIIGTATFYQYVSVRRNHRSSGSVNTACHFNMAOGLTLGTMDOQIYAVEGYFS 181
QY 182 SSGSASITVS 190
Db 182 SSGSASITVS 190

RESULT 14

AA018647
ID AA018647 standard; protein; 190 AA.
XX
XX AA018647;
AC
XX 29-AUG-2003 (revised)
DT 24-OCT-2002 (first entry)
XX
XX T reesei xyn II xylanase.
DE
XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;
KM liquid clarification; coffee extraction; plant oil extraction;
KM starch extraction; food thickener; animal food additive; mutan; mutein.
XX
XX Hypocrea jecorina.
OS
XX WO200238746-A2.
XX
XX 16-MAY-2002.
XX
XX 09-NOV-2001; 2001WO-US048018.
XX
XX 10-NOV-2000; 2000US-00710050.
XX
XX (XENC-) XENCOR INC.
XX
XX Bentzien J, Dahiyat B;
XX
XX WPI; 2002-608200/65.
XX
XX Novel xylanase activity protein, useful in bleaching process of pulp and
PT in food and animal feed industry, has enhanced thermostability and
PT alkalophilicity.
XX
XX Disclosure; Fig 16f; 121pp; English.
PS
XX The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability.
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickeners, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention. (Updated on 29-AUG-
CC 2003 to standardise OS field)
XX
SQ Sequence 190 AA;

Query Match 96.7%; Score 1021; DB 5; Length 190;
Best Local Similarity 98.4%; Pred. No. 1.5e-86;
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TIOFGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVNMNSGNFVGGKGMQPGTKNKVIN 61
Db 2 TIQGTGYNNGFYFYSYVNDGSGVYTYNNGPGGQPSVNMNSGNFVGGKGMQPGTKNKVIN 61
QY 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKIGEVTCCGSVYDIYRTQ 121
Db 62 FSGSYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPGTGATKIGEVTCCGSVYDIYRTQ 121
QY 122 RVNPSIIIGTATFYQYVSVRRNHRSSGSVNTACHFNMAOGLTLGTMDOQIYAVEGYFS 181
Db 122 RVNPSIIIGTATFYQYVSVRRNHRSSGSVNTACHFNMAOGLTLGTMDOQIYAVEGYFS 181
QY 182 SSGSASITVS 190
Db 182 SSGSASITVS 190

Db 182 SSGSASITVS 190

RESULT 15

AAO30304 ID AAO30304 standard; protein; 190 AA.

XX AAO30304;

AC AAO30304;

XX 03-SEP-2003 (first entry)

DE Trichoderma reesei xylanase II mutant protein (N11D).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;

KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

XX Hypocrea jecorina.

OS Synthetic.

XX Key Location/Qualifiers

XX MISC-difference 11 /note= "Wild type Asn substituted with Asp"

XX W02003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WC-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANA) NAT RES COUNCIL CANADA.

XX Sung WL;

XX WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved

XX thermophilicity, alkalophilicity and expression efficiency, in comparison

XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page: 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved

XX thermophilicity, alkalophilicity and expression efficiency, in comparison

XX to a corresponding native xylanase from Trichoderma reesei. The modified

XX xylanase is useful in an industrial process e.g. pulp manufacturing. It

XX is useful for the bleaching of pulp, processing of precision devices and

XX for improving digestibility of poultry and swine feed. The present

XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This

XX sequence is not shown in the specification but is derived from

XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16

XX in Figure 2 of the specification (AAO30259)

XX SQ Sequence 190 AA;

XX Query Match 96.7%; Score 1021; DB 7; Length 190;

XX Best Local Similarity 97.9%; Pred. No. 1,5e-86;

XX Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

XX 1 OTIQPGTYNNGYFYSYWMDGHTVYTNPGGQFSYWNMSNGNPFYGGKMGQPGTKNKYI 60

XX 1 OTIQPGTYNDGIFYSYWMDGHTVYTNPGGQFSYWNMSNGNPFYGGKMGQPGTKNKYI 60

XX 61 NFGSYNPNNGNSYISVYWGSRNPLIEYIYVENFTYNPSTGATKLGAVTCDSVYDIYRT 120

XX 61 NFGSYNPNNGNSYISVYWGSRNPLIEYIYVENFTYNPSTGATKLGAVTCDSVYDIYRT 120

XX 121 QRVNQPFIIGTATFYQYWSVRNRRSSGVNTACHFVAMQHGTLTGTMQYQIVAVEGYF 180

XX 121 QRVNQPFIIGTATFYQYWSVRNRRSSGVNTACHFVAMQHGTLTGTMQYQIVAVEGYF 180

XX 181 SSGSASITVS 190

Db 181 SSGSASITVS 190

Search completed: June 30, 2004, 19:39:27
Job time : 48.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds
(without alignments)
700.638 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056

Sequence: 1 QTIQPGTGNNGNYGYRYWMD.....YQIVAVGEGFSSGSASTVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1026	97.2	190	1	US-08-044-621D-26
2	1026	97.2	190	1	US-08-709-912-16
3	1026	97.2	190	2	US-09-047-370-16
4	1026	97.2	223	2	US-08-121-436A-2
5	1021	96.7	190	4	US-09-570-856B-22
6	1016	96.2	190	1	US-08-709-912-17
7	1016	96.2	190	2	US-09-047-370-17
8	1013	95.9	190	1	US-08-044-621D-27
9	1010	95.6	223	3	US-09-254-733-7
10	1003	95.0	190	4	US-09-570-856B-19
11	990	93.8	190	1	US-08-044-621D-28
12	990	93.8	190	1	US-08-709-912-14
13	990	93.8	190	4	US-09-047-370-14
14	984	93.2	190	4	US-09-570-856B-20
15	709.5	67.2	261	3	US-08-768-373-2
16	709.5	67.2	261	4	US-09-849-212A-2
17	661.5	62.6	225	4	US-09-570-856B-26
18	656.5	62.2	225	3	US-08-886-765-2
19	656.5	62.2	225	3	US-09-115-660-2
20	651.5	61.7	194	4	US-09-570-856B-24
21	650.5	61.6	225	1	US-08-290-979A-8
22	644.5	61.0	194	4	US-09-570-856B-23
23	644.5	60.8	221	4	US-09-570-856B-29
24	640.5	60.7	230	3	US-08-768-373-4
25	640.5	60.7	230	4	US-09-849-242A-4
26	632.5	59.9	223	4	US-09-462-246-2
27	625	59.2	226	4	US-09-367-891A-2

28	617.5	58.5	227	1	US-08-458-023B-4	Sequence 4, Appl1
29	615	58.2	231	2	US-08-902-655A-6	Sequence 6, Appl1
30	615	58.2	296	1	US-08-507-431-6	Sequence 6, Appl1
31	615	58.2	296	3	US-09-116-622-6	Sequence 6, Appl1
32	615	58.2	296	3	US-09-219-277-6	Sequence 6, Appl1
33	615	58.2	296	3	US-09-599-661-6	Sequence 6, Appl1
34	604.5	57.2	189	1	US-08-709-912-13	Sequence 13, Appl1
35	604.5	57.2	189	2	US-09-047-370-13	Sequence 13, Appl1
36	586.5	55.5	197	1	US-08-044-621D-29	Sequence 29, Appl1
37	586.5	55.5	197	1	US-08-709-912-9	Sequence 9, Appl1
38	586.5	55.5	197	2	US-09-047-370-9	Sequence 9, Appl1
39	586.5	55.5	197	4	US-09-570-856B-18	Sequence 18, Appl1
40	583.5	55.3	344	2	US-08-468-812-2	Sequence 2, Appl1
41	583.5	55.3	344	4	US-08-590-563-2	Sequence 2, Appl1
42	583.5	55.3	344	4	US-09-770-621-2	Sequence 2, Appl1
43	583.5	55.3	344	4	US-09-835-832-2	Sequence 2, Appl1
44	576	54.5	206	1	US-08-315-695-19	Sequence 19, Appl1
45	576	54.5	215	1	US-08-044-621D-34	Sequence 34, Appl1

ALIGNMENTS

RESULT 1
US-08-044-621D-26
Sequence 26, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Gowling, Strathly & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Bratc
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No

FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21KD, PI 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torronene, A., Mach, R. L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.,
AUTHORS: & Kudrick, C.P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 97.2%; Score 1026; DB 1; Length 190;
Best Local Similarity 98.4%; Pred. No. 1.1e-88;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNPGGQFVYVWSNSGNFVGKGMQPGTKXKI 60
DB 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNPGGQFVYVWSNSGNFVGKGMQPGTKXKI 60
QY 61 NFSGSYNPNNGNSYLSVYSGSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYSGSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQVSVVRNHRSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQVSVVRNHRSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kudrick, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 97.2%; Score 1026; DB 1; Length 190;
Best Local Similarity 98.4%; Pred. No. 1.1e-88;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNPGGQFVYVWSNSGNFVGKGMQPGTKXKI 60
DB 1 QTIQPGTGYNNNGFYFSYNNNDGCGVYTYNPGGQFVYVWSNSGNFVGKGMQPGTKXKI 60
QY 61 NFSGSYNPNNGNSYLSVYSGSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYSGSRNPLIEYIVENFGTYNPGTATKLGCVTSQSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQVSVVRNHRSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQVSVVRNHRSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSER: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren R.
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039-2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Mach, R. J.
AUTHORS: Messner, R.
AUTHORS: Gonzalez, R.
AUTHORS: Kalkinen, N.
AUTHORS: Hakki, A.
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 97.2%; Score 1026; DB 2; Length 190;
Best Local Similarity 98.4%; Pred. No. 1.3e-88;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 QTIQPGTGYNNGYFYSYVNDHGCVTYTNGPGQGFVSVMNSGNFVGKGMQPGTKNKVI 60
Db 1 QTIQPGTGYNNGYFYSYVNDHGCVTYTNGPGQGFVSVMNSGNFVGKGMQPGTKNKVI 60
QY 61 NFSSSYNPNNGSYLSYVGMKSNPLIEYIYVENFGTYNPSGTATLGEVTSDDGSYVDIYRT 120
Db 61 NFSSSYNPNNGSYLSYVGMKSNPLIEYIYVENFGTYNPSGTATLGEVTSDDGSYVDIYRT 120
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 180
Db 121 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
```

RESULT 4
US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Riitta
APPLICANT: Paloheimo, Marja
APPLICANT: Lantinen, Tarja
APPLICANT: Fagerster m, Richard
TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Keeseler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 97.2%; Score 1026; DB 2; Length 223;
Best Local Similarity 98.4%; Pred. No. 1.3e-88;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 QTIQPGTGYNNGYFYSYVNDHGCVTYTNGPGQGFVSVMNSGNFVGKGMQPGTKNKVI 60
Db 34 QTIQPGTGYNNGYFYSYVNDHGCVTYTNGPGQGFVSVMNSGNFVGKGMQPGTKNKVI 93
QY 61 NFSSSYNPNNGSYLSYVGMKSNPLIEYIYVENFGTYNPSGTATLGEVTSDDGSYVDIYRT 120
Db 61 NFSSSYNPNNGSYLSYVGMKSNPLIEYIYVENFGTYNPSGTATLGEVTSDDGSYVDIYRT 120
QY 121 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 180
Db 121 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 180
QY 154 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 213
Db 154 QRVNQPSSIIGTATFYQYWSVRRNRSSGSVNTACHFNAMAQHGTLTGTMVQIYAVEGYF 213
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
```

RESULT 5
US-09-570-856B-22

Sequence 22, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M.
APPLICANT: Dahljat, Basail I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/MS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133, 714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3*"
US-09-570-856B-22

Query Match 96.7%; Score 1021; DB 4; Length 190;
Best Local Similarity 98.4%; Pred. No. 3,1e-88;
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TIPOGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNWMSNGNFVGSKGQPGTKNVI 61
DB 2 TIPOGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNWMSNGNFVGSKGQPGTKNVI 61
QY 62 FSGSYNPNNGSYLVYSGSRNPLIEYIVENFGTYNPGTATKLGVTCCGSVYDIYRTQ 121
DB 62 FSGSYNPNNGSYLVYSGSRNPLIEYIVENFGTYNPGTATKLGVTSSGSVYDIYRTQ 121
QY 122 RVNQPSTIGTATFYQYMSVRRNRSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 181
DB 122 RVNQPSTIGTATFYQYMSVRRNRSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 181
QY 182 SSGASITVS 190
DB 182 SSGASITVS 190

RESULT 6
US-08-709-912-17
Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
-AUTHORS: Roy, C
AUTHORS: Ujle, M
AUTHORS: Watson, D. C.
AUTHORS: Makarchuk, M.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match 96.2%; Score 1016; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 9,1e-88;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIPOGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNWMSNGNFVGSKGQPGTKNVI 60
DB 1 QTIPOGTGNNNGYFYSYNDGSGVYTNNGPGQFSVNWMSNGNFVGSKGQPGTKNVI 60
QY 61 NFSGSYNPNNGSYLVYSGSRNPLIEYIVENFGTYNPGTATKLGVTSSGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLVYSGSRNPLIEYIVENFGTYNPGTATKLGVTSSGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYMSVRRNRSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYMSVRRNRSSGSVNTACHFNMAOGLTLGMDYQIYAVEGYF 180
QY 181 SSGASITVS 190
DB 181 SSGASITVS 190

RESULT 7
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:

APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen M., Warren E.
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujile, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 96.2%; Score 1016; DB 2; Length 190;
Best Local Similarity 97.4%; Pred. No. 9.1e-88;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFSSYNNNDHGVTYNNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 OTIQPGTGFNNNGYFSSYNNNDHGVTYNNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEIYIVENFGTYNPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEIYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 ORVNOPSTIGTATFYQWMSVRNRHSSGSVNTACHFNMAHQGLTGTMDYQIYAVEGYF 180
DB 121 ORVNOPSTIGTATFYQWMSVRNRHSSGSVNTACHFNMAHQGLTGTMDYQIYAVEGYF 180
QY 181 SSGASATVS 190
DB 181 SSGASATVS 190

RESULT 8
US-08-044-621D-27
Sequence 27, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:

ADDRESSER: Gowling, Strathby & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erralt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
STRAIN: Trichoderma viride, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
AUTHORS: D.C. & Wakarchuk W.
TITLE: Amino Acid Sequence of the Low-Molecular-
TITLE: Weight Xylanase from Trichoderma viride
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 149-154
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-27

Query Match 95.9%; Score 1013; DB 1; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.7e-87;
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIQPGTGYNNNGYFSSYNNNDHGVTYNNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 OTIQPGTGFNNNGYFSSYNNNDHGVTYNNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEIYIVENFGTYNPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEIYIVENFGTYNPSTGATKLGCVTSDGSVYDIYRT 120
QY 121 ORVNOPSTIGTATFYQWMSVRNRHSSGSVNTACHFNMAHQGLTGTMDYQIYAVEGYF 180
DB 121 ORVNOPSTIGTATFYQWMSVRNRHSSGSVNTACHFNMAHQGLTGTMDYQIYAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSSVNTANHFNAQAQGLTLGTMQYIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 9
 US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ; GENERAL INFORMATION:
 ; APPLICANT: MATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORU
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: MURAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
 ; FILE REFERENCE: 99-0266*/LC(IMC)/00144
 ; CURRENT APPLICATION NUMBER: US/09/254,733
 ; CURRENT FILING DATE: 1999-05-07
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1
 US-09-254-733-7

Query Match 95.6%; Score 1010; DB 3; Length 223;
 Best Local Similarity 96.3%; Pred. No. 4.1e-87;
 Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYNNDGAGVYTNNGPGQGFVWMSNSGNFVGKGMQPGTKKVI 60
 Db 34 QTIQPGTGNNNGYFYSYNNDGAGVYTNNGPGQGFVWMSNSGNFVGKGMQPGTKKVI 93
 QY 61 NFSGTYNPNNGSYLSVYGMRSNPLIEYIVENFGYNPSTGATKLGCVTCDSVYDIYRT 120
 Db 94 NFSGTYNPNNGSYLSVYGMRSNPLIEYIVENFGYNPSTGATKLGCVTCDSVYDIYRT 153
 QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAAGHGLTGMQYIVAVEGYF 180
 Db 154 QRVNPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAAGHGLTGMQYIVAVEGYF 213
 QY 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 10
 US-09-570-856B-19
 ; Sequence 19, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570,856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133,714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Trichoderma viride
 US-09-570-856B-19

Query Match 95.0%; Score 1003; DB 4; Length 190;
 Best Local Similarity 95.8%; Pred. No. 1.5e-86;
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNNGYFYSYNNDGAGVYTNNGPGQGFVWMSNSGNFVGKGMQPGTKKVI 60
 Db 1 QTIQPGTGNNNGYFYSYNNDGAGVYTNNGPGQGFVWMSNSGNFVGKGMQPGTKKVI 60
 QY 61 NFSGTYNPNNGSYLSVYGMRSNPLIEYIVENFGYNPSTGATKLGCVTCDSVYDIYRT 120
 Db 61 NFSGTYNPNNGSYLSVYGMRSNPLIEYIVENFGYNPSTGATKLGCVTCDSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAAGHGLTGMQYIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSSVNTACHFNMAAAGHGLTGMQYIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 11
 US-08-044-621D-28
 ; Sequence 28, Application US/08044621D
 ; Patent No. 5405769
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren W. Makarchuk
 ; APPLICANT: Wang L. Sung
 ; APPLICANT: Makoto Yaguchi
 ; APPLICANT: Robert L. Campbell
 ; APPLICANT: David R. Rose
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 ; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gowing, Strachy & Henderson
 ; STREET: Suite 2600, 160 Elgin Street
 ; CITY: Ottawa
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: K1P 1C3
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 ; OPERATING SYSTEM: IBM PC
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/044,621D
 ; FILING DATE: April 8, 1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Judy A. Eizalt
 ; REGISTRATION NUMBER: 34,076
 ; REFERENCE/DOCKET NUMBER: 08-863796
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 613-786-0199
 ; TELEFAX: 613-563-9869
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 190
 ; TYPE: Amino Acid
 ; STRANDEDNESS: No. 5405769 Relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: protein
 ; HYPOTHEICAL: No
 ; ANTI-SENSE: No
 ; FRAGMENT TYPE: No
 ; ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum
 STRAIN: Trichoderma harzianum, 20KD
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
 AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
 AUTHORS: J.N.
 TITLE:
 JOURNAL: Xylans and Xylanases
 VOLUME:
 ISSUE:
 PAGES: 435-438
 DATE: 1992
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-28

Query Match 93.8%; Score 990; DB 1; Length 190;
 Best Local Similarity 94.2%; Pred. No. 2.5e-85;
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYYSVYVNDGHHGVTYTNPGGQFVYVMSNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYNNGYFYYSVYVNDGHHGVTYTNPGGQFVYVMSNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSYVYVMSNRNPLEIYIVENFGTYNPSTGATKGEVTCDSGYVDIYRT 120
 DB 61 NFSGSYNPNNGSYLSYVYVMSNRNPLEIYIVENFGTYNPSTGATKGEVTCDSGYVDIYRT 120
 QY 121 QRVNPSITIGTATFYVYVMSVRNRHSSGSVNTACHPNMAOCHGLTLGTMDOYIVAVEGYF 180
 DB 121 QRVNPSITIGTATFYVYVMSVRNRHSSGSVNTACHPNMAOCHGLTLGTMDOYIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 12
 US-08-709-912-14
 Sequence 14, Application US/08709912
 Patent No. 5759840
 GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen KF, Warren E
 REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma harzianum
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi, M
 AUTHORS: Watson, D. C.
 AUTHORS: Roy, C
 AUTHORS: Rollin, F
 AUTHORS: Tan, L. U. L.
 AUTHORS: Senior, D. J.
 AUTHORS: Saddler, J. N.
 JOURNAL: Xylan and Xylanase
 PAGES: 435-438
 DATE: 1992
 US-08-709-912-14

Query Match 93.8%; Score 990; DB 1; Length 190;
 Best Local Similarity 94.2%; Pred. No. 2.5e-85;
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYYSVYVNDGHHGVTYTNPGGQFVYVMSNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYNNGYFYYSVYVNDGHHGVTYTNPGGQFVYVMSNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLSYVYVMSNRNPLEIYIVENFGTYNPSTGATKGEVTCDSGYVDIYRT 120
 DB 61 NFSGSYNPNNGSYLSYVYVMSNRNPLEIYIVENFGTYNPSTGATKGEVTCDSGYVDIYRT 120
 QY 121 QRVNPSITIGTATFYVYVMSVRNRHSSGSVNTACHPNMAOCHGLTLGTMDOYIVAVEGYF 180
 DB 121 QRVNPSITIGTATFYVYVMSVRNRHSSGSVNTACHPNMAOCHGLTLGTMDOYIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 13
 US-09-047-370-14
 Sequence 14, Application US/09047370
 Patent No. 5866408
 GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wing L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Oisen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match 93.8%; Score 990; DB 2; Length 190;
Best Local Similarity 94.2%; Pred. No. 2,5e-85;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVWSNSGNFVGGKMQPGTKXKI 60
DB 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVWSNSGNFVGGKMQPGTKXKI 60
QY 61 NFSGSYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAOCHGLTLGTMDOYIVAVEGYF 180
DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAOCHGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Bentzien, Basill I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

Query Match 93.2%; Score 984; DB 4; Length 190;
Best Local Similarity 93.7%; Pred. No. 9.1e-85;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVWSNSGNFVGGKMQPGTKXKI 60
DB 1 QTIQPGTGYNNNGFYFVYVNDGHHGVTYTNPGGQFVYVWSNSGNFVGGKMQPGTKXKI 60
QY 61 NFSGSYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGMRSRNPLEYIYVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
QY 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAOCHGLTLGTMDOYIVAVEGYF 180
DB 121 QRVNQPSTIIGTATFYQYVSVRRNRHSSGSVNTACHFNMAOCHGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VERMANPER, JARI
APPLICANT: LANTTO, RAIIA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHELE A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,0540003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURES:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= XLNA
US-08-766-373-2

Query Match 67.2%; Score 709.5; DB 3; Length 261;

Best Local Similarity 65.3%; Pred. No. 7.4e-59;

Matches 124; Conservative 27; Mismatches 38; Indels 1; Gaps 1;

QY	1	QTI-QPTGYNNNGYFYSYNDGAGVTYTNPGGQFSSYNNNSNGNPFYGGKGMOPGTNKY	59
DB	27	QTLTSATGTHNGYYSFTWTDGQGNIRFNLESQGYSTWNGNNGWVGKGMNPGTDNRV	86
QY	60	INFGSTNPNGNSYLSVYGMARNPLIEYIYENFGTYNPSTGATKLGVTCDGSVDIYR	119
DB	87	INYADYRPNNGNSYLAAYGWTNRNPLIEYVYESFGTYDPSGTATRMGSVTTDGGTYNIYR	146
QY	120	TORVNOPIIGTATFYCYWSYRNRHSSGSVNTACHFNAMQHGLTGMTDYQIYAEGY	179
DB	147	TORVNPISIBGIXTFYQIWSYRISKRTGTVTMNHFNMARQAGLQLSHDIQIVATEGY	206
QY	180	FSSGSASITV	189
DB	207	YSSGSATVNV	216

Search completed: June 30, 2004, 19:44:47
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)
1441.987 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056
Sequence: 1 QTIQPTGTGNGYFYSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1166195 segs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	190	US-10-307-441-16	Sequence 16, Appl
2	1026	97.2	222	US-10-237-386-32	Sequence 32, Appl
3	1026	97.2	223	US-10-237-386-31	Sequence 31, Appl
4	1016	96.2	190	US-10-307-441-17	Sequence 17, Appl
5	1014	96.0	223	US-10-237-386-30	Sequence 30, Appl
6	990	93.8	190	US-10-307-441-14	Sequence 14, Appl
7	984	93.2	190	US-10-237-386-33	Sequence 33, Appl
8	869	82.3	223	US-10-237-386-34	Sequence 34, Appl
9	764.5	72.4	241	US-10-237-386-35	Sequence 35, Appl
10	703.5	66.6	219	US-10-237-386-29	Sequence 29, Appl
11	676.5	64.1	227	US-10-237-386-22	Sequence 22, Appl
12	670.5	63.5	227	US-10-237-386-21	Sequence 21, Appl
13	670	63.4	313	US-10-213-990-72	Sequence 72, Appl
14	663.5	62.8	234	US-10-213-990-69	Sequence 69, Appl
15	656.5	62.2	189	US-10-307-441-19	Sequence 19, Appl

16	656.5	62.2	194	US-10-307-441-20	Sequence 20, Appl
17	656.5	62.2	225	US-09-467-368-2	Sequence 2, Appl
18	656.5	62.2	225	US-10-237-386-24	Sequence 24, Appl
19	654.5	62.0	221	US-10-213-990-66	Sequence 66, Appl
20	649.5	61.5	225	US-10-237-386-36	Sequence 36, Appl
21	642.5	60.8	221	US-10-237-386-20	Sequence 20, Appl
22	641	60.7	221	US-10-237-386-37	Sequence 37, Appl
23	632.5	59.9	223	US-10-299-393-2	Sequence 2, Appl
24	632	59.8	223	US-09-790-070A-11	Sequence 11, Appl
25	627.5	59.4	231	US-10-237-386-26	Sequence 26, Appl
26	620.5	58.8	231	US-10-237-386-25	Sequence 25, Appl
27	614.5	58.2	221	US-10-237-386-44	Sequence 44, Appl
28	611.5	57.9	227	US-10-237-386-27	Sequence 27, Appl
29	604.5	57.2	189	US-10-307-441-13	Sequence 13, Appl
30	604.5	57.2	240	US-10-237-386-42	Sequence 42, Appl
31	603.5	57.1	239	US-10-237-386-40	Sequence 40, Appl
32	602.5	57.1	241	US-10-237-386-43	Sequence 43, Appl
33	596	56.4	228	US-10-237-386-45	Sequence 45, Appl
34	587	55.6	216	US-10-237-386-39	Sequence 39, Appl
35	586.5	55.5	197	US-10-307-441-9	Sequence 9, Appl
36	586.5	55.5	201	US-10-237-386-23	Sequence 23, Appl
37	583.5	55.3	344	US-09-770-621-2	Sequence 2, Appl
38	583.5	55.3	344	US-10-286-993-2	Sequence 2, Appl
39	578.5	54.8	242	US-10-237-386-41	Sequence 41, Appl
40	574	54.4	191	US-10-307-441-10	Sequence 10, Appl
41	565.5	53.6	233	US-10-237-386-28	Sequence 28, Appl
42	523.5	49.6	226	US-10-237-386-63	Sequence 63, Appl
43	520.5	49.3	232	US-10-237-386-64	Sequence 64, Appl
44	520.5	49.3	237	US-10-237-386-47	Sequence 47, Appl
45	512.5	48.5	189	US-10-307-441-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-307-441-16
; Sequence 16, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 02767-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-307-441-16
Query Match 97.2% Score 1026; DB 14; Length 190;
Best Local Similarity 98.4%; Pred. No. 2.5e-93;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 QTIQPTGTGNGYFYSYNDHGAGVTYNGGSGPVSWSNGVFGKGMOPGKMYI 60
Db 1 QTIQPTGTGNGYFYSYNDHGAGVTYNGGSGPVSWSNGVFGKGMOPGKMYI 60
QY 61 NFSGSYNGNSYLSVYGSNRPILBYIVNFGYNPSTGATKLGVEYTCGSYVDYRT 120
Db 61 NFSGSYNGNSYLSVYGSNRPILBYIVNFGYNPSTGATKLGVEYTCGSYVDYRT 120
QY 121 QYVNPSTIGATPFQVYSVRNRHSSGSYVTACHFNMAQHGLTGMDCQIVAVEGYF 180

Db 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 2
US-10-237-386-32
; Sequence 32, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-32

Query Match 97.2%; Score 1026; DB 14; Length 222;
Best Local Similarity 98.4%; Pred. No. 3.1e-93;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 60
Db 33 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 92
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120
Db 93 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 152
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 180
Db 153 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 212
QY 181 SSGSASITVS 190
Db 213 SSGSASITVS 222

RESULT 3
US-10-237-386-31
; Sequence 31, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-31

Query Match 97.2%; Score 1026; DB 14; Length 223;
Best Local Similarity 98.4%; Pred. No. 3.1e-93;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 60
Db 34 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 93
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120
Db 94 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 153
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 180
Db 154 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 4
US-10-307-441-17
; Sequence 17, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Ming L.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; TITLE OF INVENTION: and AlphaLophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma viride
US-10-307-441-17

Query Match 96.2%; Score 1016; DB 14; Length 190;
Best Local Similarity 97.4%; Pred. No. 2.5e-92;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 60
Db 1 OTIOPGTGNNNGFYFYSYNDGHHGVTYTNPGGQFYSVWMSNSGNFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120
Db 61 NFSGSYNPNNGSYLSVYGMRSNPLIEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 180
Db 121 QRVNPSIIGTATFYQVSVRRNRSSGSVNTAHFNMAAQGLTLGTMDOIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 5
US-10-237-386-30
; Sequence 30, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-30

Query Match 96.0%; Score 1014; DB 14; Length 223;
Best Local Similarity 97.4%; Pred. No. 4,8e-92;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 60
DB 34 QTIQPGTGNNGYFYSHYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 93
QY 61 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120
DB 94 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 153
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180
DB 154 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTAHNFMAAQQGLTLGTMDYQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 6
US-10-307-441-14
; Sequence 14, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Ming L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769,
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match 93.8%; Score 990; DB 14; Length 190;
Best Local Similarity 94.2%; Pred. No. 9,2e-90;

Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGNNGYFYSHYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTAHNFMAAQQGLTLGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-10-237-386-33
; Sequence 33, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRT
; ORGANISM: T. harzianum
US-10-237-386-33

Query Match 93.2%; Score 984; DB 14; Length 190;
Best Local Similarity 93.7%; Pred. No. 3,6e-89;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGNNGYFYSHYVNDHGVTYTNNGPGGQSYVMSNSGNFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLVYSGMSRNPLEYIYVENFGTYNPSTGATKLGVTSDGSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNAMAQGLTLGTMDYQIYAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQYWSVRNRHSSGSVNTAHNFMAAQQGLTLGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8
US-10-237-386-34
; Sequence 34, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole


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? PRIOR APPLICATION NUMBER: PCT/IS01/00426
? PRIOR FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: GB 0005585.5
? PRIOR FILING DATE: 2000-03-08
? PRIOR APPLICATION NUMBER: GB 0015751.1
? PRIOR FILING DATE: 2000-06-27
? NUMBER OF SEQ ID NOS: 66
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 22
? LENGTH: 227
? TYPE: PR1
? ORGANISM: A. pist
US-10-237-386-22

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Query Match	64.1%;	Score 676.5;	DB 14;	Length 227;
Best Local Similarity	65.3%;	Pred. No. 1.1e-58;		
Matches 126;	Conservative 20;	Mismatches 42;	Indels 5;	Gaps 2;

QY	2	TIQGT-----	TNNNGYFYSYNNDDHGAGLYTNNPGGCGSNNVMSNSGNFVGGGQWPGTKN	57
		:	:	
Db	34	TARGTBSQGTHTGCGFYSWMTDGAQATYTNAGAGSISVNMKKTGNNVGGKGNPFGAA-	92	
		:	:	
QY	58	KVINPSSGYNENGNSSYLSVYGMNRNPLEEYIVENFGYENPBTGATKLGEVYCDGSVYDI	117	
		:	:	
Db	93	RTIYSGSYSPSSGNSYLAVYGMTRNPLEEYVEEFGYIVDPSSQATVAGSVTAQDSSYKI	152	
		:	:	
QY	118	YRTQPVNDPSLIGTATFYQYWSVRRNRHSSGGSVNTACHPNMAOGLTLGTMDYQIVAVE	177	
		:	:	
Db	153	AQRTRTNPSSIDGTQTFQOYWSVPRNKSSGGSVNMKTHFDMAAKMKLGITHNYQIVATE	212	
		:	:	
QY	178	GYFSSGSAITVVS	190	
		:	:	
Db	213	GYFSSGSAQITVN	225	
		:	:	

RESULT 12
 US-10-237-386-21
 ; Sequence 21. Application US/10237386
 ; Publication No. US20030180895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Danisco A/S
 ; APPLICANT: Slibesen, Ole
 ; APPLICANT: Sorensen, Jens
 ; TITLE OF INVENTION: Xylanse Variants Having Altered Sensitivity to Xylanase Inhibitor
 ; FILE REFERENCE: 674509-2046
 ; CURRENT APPLICATION NUMBER: US/10/237,386
 ; CURRENT FILING DATE: 2002-12-06
 ; PRIOR APPLICATION NUMBER: PCT/IB01/00426
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: GB 0005585.5
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: GB 0015751.1
 ; PRIOR FILING DATE: 2000-06-27
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: patentIn version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: H. turcicum
 ; US-10-237-386-21

Query Match	63.5%;	Score 670.5;	DB 14;	Length 227;
Best Local Similarity	64.2%;	Pred. No. 4.4e-58;		
Matches 122;	Conservative 22;	Mismatches 45;	Indels 1;	Gaps 1;

Qy 1 TTIDPQTGYNNYGFPSYNNDDGGVATYNNPGGQCSYNNMSNGNVGKGKGMPEYKKNYI 60
Db 37 QSTNGEBETHNGCFPSWMSDDGARATYNNAGGAGSYSVEMGTGCGNIVGKGMNPGTA RTI 95
Qy 61 NFGSGSYNNNGNSYLSYVGKSRNPLEYIVENFGYNNSTGATKKGAVTCDGASYDIYRT 120
Db 96 TYSGGYNNNGNSYLAIVGMTNPLEYEVVENFGYNNSTGATKKGAVTCDGASYDIYRT 155

Qy	Db	Qy	Db
121	156	181	216
Q R N C S E I I G L T A T F Y Y W M V R N H S S G S V N T A C H E N M A O H G L T T M D Y Q I A V E G Y F	T R N G S I D I G T R F Q Q Y S V R Q N K R S S G S V M K K H F D M A S K G N L S H Y Q I A T E G Y F	S G S G S A S I T V S	S G S G S A S I T V N
180	215	190	225

```

RESULT 13
US-10-213-990-72
; Sequence 72, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:

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1  APPLICANT:  Bussey, Howard
2  APPLICANT:  Storms, Reg
3  APPLICANT:  Roemer, Terry
4  TITLE OF INVENTION:  NUCLEIC ACIDS OF ASPERGILLUS FMIGIGATUS ENCODING INDUSTRIAL
5  TITLE OF INVENTION:  ENZYMES AND METHODS OF USE
6  FILE REFERENCE:  10182-019-999
7  CURRENT APPLICATION NUMBER:  US/10/213,990
8  CURRENT FILING DATE:  2002-08-05
9  NUMBER OF SEQ ID NOS:  72
10 SOFTWARE:  FastSeq for Windows Version 4.0
11 SEQ ID NO 72
12 LENGTH:  313
13 TYPE:  PRF
14 ORGANISM:  Aspergillus
15 OS-10-213-990-72

```

Query Match	63.4%	Score 670;	DB 14;	Length 313;
Best Local Similarity	63.2%	Pred. No. 7.3e-58;		
Matches 122;	Conservative 29;	Mismatches 38;	Indels 4;	Gaps 3;

[illegible]

RESULT 14
US-10-213-990-69
; Sequence 69, Application US/10213990
; Publication NO. US20030082595A1

```

1  APPLICANT: Bussey, Howard
2  APPLICANT: Storms, Reg
3  APPLICANT: Roemer, Terry
4  TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS ENCODING INDUSTRIAL
5  TITLE OF INVENTION: ENZYMES AND METHODS OF USE
6  FILE REFERENCE: 10182-019-.999
7  CURRENT APPLICATION NUMBER: US/10/213,.990
8  CURRENT FILING DATE: 2002-08-05
9  NUMBER OF SEQ ID NOS: 72
10 SOFTWARE: FastSeq for Windows Version 4.0
11 SEQ ID NO 69
12 LENGTH: 234
13 TYPE: PRT
14 ORGANISM: Aspergillus

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:39 ; Search time 13 Seconds
(without alignments)
1405.876 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056

Sequence: 1 QTIQPGTGYNGYFYGYWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1026	97.2	222	2 S39154	xylinase 1 - fungus
2	1026	97.2	223	2 S39883	endo-1,4-beta-xylinase
3	1003	95.0	190	1 A44594	endo-1,4-beta-xylinase
4	999	94.6	190	1 A44595	endo-1,4-beta-xylinase
5	990	93.8	190	1 A44593	endo-1,4-beta-xylinase
6	764.5	72.4	241	2 S71473	endo-1,4-beta-xylinase
7	703.5	66.6	219	2 S71472	endo-1,4-beta-xylinase
8	690.5	65.4	232	2 JCT577	endo-1,4-beta-xylinase
9	669.5	63.4	225	1 S57477	endo-1,4-beta-xylinase
10	655.5	62.1	221	1 S57469	endo-1,4-beta-xylinase
11	641	60.7	221	2 JCT307	endo-1,4-beta-xylinase
12	611.5	57.9	227	2 S43919	endo-1,4-beta-xylinase
13	586.5	55.5	197	1 A44597	endo-1,4-beta-xylinase
14	576	54.5	333	1 T50590	endo-1,4-beta-xylinase
15	576	54.5	335	2 J50601	endo-1,4-beta-xylinase
16	559.5	53.0	644	1 I40712	endo-1,4-beta-xylinase
17	530.5	49.3	661	1 S59633	endo-1,4-beta-xylinase
18	515.2	48.8	241	2 T37005	endo-1,4-beta-xylinase
19	512	48.3	240	1 J50591	endo-1,4-beta-xylinase
20	510.5	48.3	656	1 S59631	endo-1,4-beta-xylinase
21	510	48.3	240	1 S47512	endo-1,4-beta-xylinase
22	509.5	48.2	210	2 C83762	endo-1,4-beta-xylinase
23	497	47.1	213	1 I40569	endo-1,4-beta-xylinase
24	496	47.0	213	1 S01734	endo-1,4-beta-xylinase
25	496	47.0	213	1 S48126	endo-1,4-beta-xylinase
26	464	43.9	354	1 S51779	endo-1,4-beta-xylinase
27	462	43.8	228	1 WMB5XP	endo-1,4-beta-xylinase
28	449.5	42.6	261	1 S12745	endo-1,4-beta-xylinase
29	436	41.3	511	1 JQ1935	endo-1,4-beta-xylinase

30	427.5	40.5	229	2 S39155	xylinase 2 - fungus
31	424.5	40.2	209	2 UC4909	endo-1,4-beta-xylinase
32	424	40.2	211	1 S46229	endo-1,4-beta-xylinase
33	422	40.0	211	1 S49542	endo-1,4-beta-xylinase
34	419	39.7	211	1 JCT198	endo-1,4-beta-xylinase
35	397	37.6	954	1 S20907	endo-1,4-beta-xylinase
36	391	37.0	789	2 S58235	endo-1,4-beta-xylinase
37	380.5	36.0	802	2 A36910	xylinase, beta(1,3)
38	377	35.7	781	2 S51592	Xylin precursor - R
39	297	28.1	607	2 S49528	endoxylinase - rum
40	297	28.1	607	2 S24754	endo-1,4-beta-xylinase
41	288.5	27.3	608	2 B53295	xylinase (EC 3.2.1
42	280	26.5	50	2 A61149	endo-1,4-beta-xylinase
43	243.5	23.1	266	1 S48865	endo-1,4-beta-xylinase
44	121.5	11.5	2817	2 B97033	uncharacterized pr
45	117.5	11.1	1053	2 B70987	probable PPE prote

ALIGNMENTS

RESULT 1
S39154
xylinase 1 - fungus (Trichoderma reesei)
C/Species: Trichoderma reesei
C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C/Accession: S39154
R/Accession: A: Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kub.
Biotechnology 10, 1461-1465, 1992
A/Title: The two major xylinases from trichoderma reesei: characterization of both enzy
A/Reference number: S39154
A/Accession: S39154
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222 <TOB>
A/Cross-references: EMBL:X69573; NID:g396563; PIDD:CAA49293.1; PIDD:g396564
C/Genetics:
A/Genes: xyln
A/Intons: 90/2
C/Superfamily: endo-1,4-beta-xylinase; endo-1,4-beta-xylinase homology
F;44-222/Domain: endo-1,4-beta-xylinase homology <XLY>

Query Match 97.2%; Score 1026; DB 2; Length 222;
Best Local Similarity 98.4%; Pred. No. 8,7e-72;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNGYFYGYWMDHGVTYNGPGGFSVWMSNGNFVGKMGQPTKKNKI 60
DB 33 QTIOPGTGYNGYFYGYWMDHGVTYNGPGGFSVWMSNGNFVGKMGQPTKKNKI 92

QY 61 NFGSYNPNNGSYLSVYGNSRNPLIEYIVENFGYNDSTGATKUGEVTCDSYDIIRT 120
DB 93 NFGSYNPNNGSYLSVYGNSRNPLIEYIVENFGYNDSTGATKUGEVTCDSYDIIRT 152

QY 121 QVNOPSTIGTATFFQVNSVRNHRSSGSVNTACHFNMAQHGTLGTMDYQIVAVEGF 180
DB 153 QVNOPSTIGTATFFQVNSVRNHRSSGSVNTACHFNMAQHGTLGTMDYQIVAVEGF 212

QY 181 SSGSASITVS 190
DB 213 SSGSASITVS 222

RESULT 2
S39883
endo-1,4-beta-xylinase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N/Alternate names: endoxylinase II
C/Species: Trichoderma reesei
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C/Accession: S39883; S39884
R/Saarelainen, R.; Palohelmo, M.; Pengerstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A/Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylinase

A:Reference number: S39883; MUID:94088442; PMID:8264524
 A:Accession: S39883
 A:Molecule type: DNA
 A:Residues: 1-223 <SAA>
 A:Cross-references: EMBL:S67387; NID:9455906; FID:AB29346.1; PID:9455907
 A:Experimental source: strain QM6a
 A:Accession: S39884
 A:Molecule type: protein
 A:Residues: 34-43;49-57;121-151;178-191 <SAP>
 C:Genetics:
 A:Gene: xln2
 A:Introns: 91/2
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 C:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-33/Domain: propeptide #status predicted <PRO>
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
 F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:71,94/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:110,121/Binding site: substrate (Tyr) #status predicted
 F:119,210/Active site: Glu #status predicted

Query Match 97.2%; Score 1026; DB 2; Length 223;
 Best Local Similarity 98.4%; Pred. No. 8.8e-72;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 60
 Db 34 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 93
 Qy 61 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120
 Db 94 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 153
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 180
 Db 154 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 213
 Qy 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 3

A44594 endo-1,4-beta-xylanase (BC 3.2.1.8) IIA - fungus (Trichoderma viride)

N:Alternate names: xylanase IIA
 C:Species: Trichoderma viride
 C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
 C:Accession: A44594
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
 A:Accession: A44594
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>

C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 C:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:77,88/Binding site: substrate (Tyr) #status predicted
 F:86,177/Active site: Glu #status predicted

Query Match 95.0%; Score 1003; DB 1; Length 190;
 Best Local Similarity 95.8%; Pred. No. 4.3e-70;
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 60

Db 1 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 60
 Qy 61 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120
 Db 61 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 120
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 180
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 180
 Qy 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 4

A44595 endo-1,4-beta-xylanase (BC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)

N:Alternate names: xylanase IIB
 C:Species: Trichoderma viride
 C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
 C:Accession: A44595
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
 A:Accession: A44595
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>

C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 C:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:86,177/Active site: Glu #status predicted
 F:126-127/Cleavage site: pro-ser (unidentified proteinase) #status predicted
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 94.6%; Score 999; DB 1; Length 190;
 Best Local Similarity 95.3%; Pred. No. 8.7e-70;
 Matches 181; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 60
 Db 1 QTTPGTGNNNGYFYSYWNDDHGVTYTNPGGQFVSVMNSGNGFVGKGMQPTKXKI 60
 Qy 61 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTCDGSYYDIYRT 120
 Db 61 NFSGYNPNNGSYLSVYGMSPNPLIEYIYVENFGTNPSTGATKLGAVTSDGSYYDIYRT 120
 Qy 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 180
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHSSGVSNTACHFNMAOHGLTLGTMDOYQIYAVEGYF 180
 Qy 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 5

A44593 endo-1,4-beta-xylanase (BC 3.2.1.8) (validated) - fungus (Trichoderma harzianum) (strain)

N:Alternate names: xylanase
 C:Species: Trichoderma harzianum
 C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
 C:Accession: A44593
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994

A:Reference number: A44593
 A:Accession: A44593
 A:Molecule type: protein

A:Residues: 1-190 <YAG>
 A:Experimental source: strain E58
 R:Campbell, R.L.; Rose, D.R.
 Submitted to the Brookhaven Protein Data Bank, June 1994
 A:Reference number: A52868; PDB:1XND
 A:Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46, A'48-190
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xyloosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:186,177/Active site: Glu #status experimental

Query Match 93.8%; Score 990; DB 1; Length 190;
 Best Local Similarity 94.2%; Pred. No. 4,3e-69;
 Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGFYYSWMDGHGVYTNPGQGFVSVMNSGNFVGKMGQGTGKVKVI 60
 Db 1 QTIQPGTYNNNGFYYSWMDGHGVYTNPGQGFVSVMNSGNFVGKMGQGTGKVKVI 60
 QY 61 NFSGSYNPNNGSYLSTGMSRNPLIEYIYVENFCTYNPSTGATKLGCVTCDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSTGMSRNPLIEYIYVENFCTYNPSTGATKLGCVTCDGSVYDIYRT 120
 QY 121 QRVNPSIIGATFYQWYSVRNRHSSGSVNTACHFANMQHGLTGTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIGATFYQWYSVRNRHSSGSVNTANHFANMQHGLTGTMDYQIVAVEGYF 180
 QY 181 SSGASITVS 190
 Db 181 SSGASITVS 190

RESULT 6
 S71473
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
 C:Species: Chaetomium gracile
 C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C:Accession: S71473; S78207
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp
 A:Reference number: S71472; MUID:96118924; PMID:8595661
 A:Accession: S71473
 A:Molecule type: DNA
 A:Residues: 1-241 <YOS>
 A:Cross-references: EMBL:D49851; NID:g1339859; PIDN:BA08650.1; PID:g1339860
 A:Accession: S78207
 A:Molecule type: protein
 A:Residues: 38-44,89-91,153-161 <YOH>
 C:Genetics:
 A:Insertions: 88/2
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
 F:43-220/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:116,207/Active site: Glu #status predicted

Query Match 72.4%; Score 764.5; DB 2; Length 241;
 Best Local Similarity 73.8%; Pred. No. 1.1e-51;
 Matches 135; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

QY 7 TGANNNGFYYSWMDGHGVYTNPGQGFVSVMNSGNFVGKMGQGTGKVKVINSGSY 66
 Db 38 TGTNNNGFYYSFWMDGQGNVQYTNAGQGVSYVMNSGNFVGKMGQGTGKVKVINSGSY 96
 QY 67 NPNNGSYLSTGMSRNPLIEYIYVENFCTYNPSTGATKLGCVTCDGSVYDIYRTQVNOP 126

Db 97 NPNNGSYLSTGMSRNPLIEYIYVENFCTYNPSTGATKLGCVTCDGSVYDIYRTQVNOP 156
 QY 127 SIIGTATFYQWYSVRNRHSSGSVNTACHFANMQHGLTGTMDYQIVAVEGYFSSGSAS 186
 Db 157 SIIGTATFYQWYSVRNRHSSGSVNTAAHFANMQHGLTGTMDYQIVAVEGYFSSGSAT 216
 QY 187 ITV 169
 Db 217 VNV 219

RESULT 7
 S71472
 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
 N:Alternate names: xylanase A
 C:Species: Chaetomium gracile
 C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C:Accession: S71472; S78206
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp
 A:Reference number: S71472; MUID:96118924; PMID:8595661
 A:Accession: S71472
 A:Molecule type: DNA
 A:Residues: 1-219 <YOS>
 A:Cross-references: EMBL:D49850; NID:g1339857; PIDN:BA08649.1; PID:g1339858
 A:Accession: S78206
 A:Molecule type: protein
 A:Residues: 31-45,82-94,152-160 <YOH>
 C:Genetics:
 A:Insertions: 81/2
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
 F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:115,206/Active site: Glu #status predicted

Query Match 66.6%; Score 703.5; DB 2; Length 219;
 Best Local Similarity 68.1%; Pred. No. 4.8e-47;
 Matches 126; Conservative 23; Mismatches 35; Indels 1; Gaps 1;

QY 6 GTGNNNGFYYSWMDGHGVYTNPGQGFVSVMNSGNFVGKMGQGTGKVKVINSGS 65
 Db 36 GTGNNNGFYYSFWMDGQGNVQYTNAGQGVSYVMNSGNFVGKMGQGTGKVKVINSGS 94
 QY 66 YNPNGSYLSTGMSRNPLIEYIYVENFCTYNPSTGATKLGCVTCDGSVYDIYRTQVNO 125
 Db 95 PSPOGNGYLAIGWQNPVLEIYVESGTYDPSSQAKFGTICQDGSSTYIAKTRVNO 154
 QY 126 PSIIIGTATFYQWYSVRNRHSSGSVNTACHFANMQHGLTGTMDYQIVAVEGYFSSSSA 185
 Db 155 PSIEGSTFTDQFWSVRNRHSSGSVNTAAHFANMQHGLTGTMDYQIVAVEGYFSSSSS 214
 QY 186 SITVS 190
 Db 215 SITVS 219

RESULT 8
 UC7577
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
 N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
 C:Species: Aspergillus oryzae
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: UC7577; PC7120
 R:Kumura, T.; Suzuki, H.; Funahashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, B.
 Biotechnol. Biochem. 64, 2734-2738, 2000
 A:Title: Molecular cloning, overexpression, and purification of a major xylanase from As
 A:Reference number: UC7577; MUID: 21077500; PMID:11210150
 A:Accession: UC7577

A:Accession: PC7086
A:Molecule type: protein
A:Residues: 32-51 <K12>
C/Genetics:
A:Gene: xynA
A:Insertions: 89/2
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match 60.7%; Score 641; DB 2; Length 221;
Best Local Similarity 60.7%; Pred. No. 3e-42;
Matches 116; Conservative 30; Mismatches 43; Indels 2; Gaps 2;

QY 1 QTIPLG-TGVNNGFYFVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXV 59
DB 32 QTIPLG-TGVNNGFYFVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXV 59
QY 60 INFSGYNPNNGNSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYR 119
DB 91 ITFEGTNPSCNAYLAYVGMWTSPLVEYTLIEDYGDINPNMSTYKKTVTSDGSVDIYE 150
QY 120 TORVNPISITGATFYQVSVRRNRSSGVNTACHFNMAOHGLTLGTMDYQIYAVEGY 179
DB 151 HQVNPQPSISGTAFCNQVMSIRQNTRSSGVTTFANHFNAWAKLGMNLGSFMYQIVSTEGY 210
QY 180 FSSGSASITVS 190
DB 211 ESSGSSTITVS 221

RESULT 12

S43919
endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
C/Species: Humicola insolens
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C/Accession: S43919
R/Dalboe, H.; Heidt-Hansen, H. P.
Mol. Gen. Genet. 243, 253-260, 1994
A/Title: A novel method for efficient expression cloning of fungal enzyme genes.
A/Reference number: S43919; MUID:94247364; PMID:8190078

A:Accession: S43919
A:Molecule type: mRNA
A:Residues: 1-227 <DNL>
A/References: EMBL:X76047; NID:9505260; PIDN:CAAS3632.1; PID:9505261
C/Genetics:
A:Gene: XYL1
C/Function:
A/Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F:121,212/Active site: Glu #status predicted

Query Match 57.9%; Score 611.5; DB 2; Length 227;
Best Local Similarity 58.8%; Pred. No. 5.7e-40;

Matches 107; Conservative 25; Mismatches 49; Indels 1; Gaps 1;

QY 8 GYNNGYYSYVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXVNFSGS 67
DB 44 GYNNGYYSYVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXVNFSGS 102
QY 68 PNGNSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRTQVNPQ 127
DB 103 PNGNGYLAAYVGMWTSPLVEYTLIEDYGDINPNMSTYKKTVTSDGSVDIYE 162
QY 128 ITGATFYQVSVRRNRSSGVNTACHFNMAOHGLTLGTMDYQIYAVEGY 187
DB 163 IDGRTFQVMSIRKNRKRVGGSVNMQNFMAWQOHGMLQOHYQVAVTEGYSSESDI 222
QY 188 TV 189

DB 223 YV 224

RESULT 13

A44597
endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)
N/Alternate names: xylanase A
C/Species: Schizophyllum commune
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 06-Dec-1996
C/Accession: A44597; S41411; A05147; S38973
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994

A/Reference number: A44593
A:Accession: A44597
A:Molecule type: protein
A:Residues: 1-197 <YAG>
A/Experimental source: strain Delmar ATCC 38548
R/Bray, M.R.; Clarke, A.J.
Eur. J. Biochem. 219, 821-827, 1994
A/Title: Identification of a glutamate residue at the active site of xylanase A from Sc
A/Reference number: S41411; MUID:94155888; PMID:7906649
A:Accession: S41411
A:Status: preliminary
A:Molecule type: protein
A:Residues: 83-123

R/Palce, M.G.; Jurasek, L.; Carpenter, M.R.; Smillie, L.B.
Appl. Environ. Microbiol. 36, 802-808, 1978
A/Reference number: A05147; MUID:79102289; PMID:32833
A:Accession: A05147
A:Molecule type: protein
A:Residues: 1-27 <PAL>
R/Oku, T.; Roy, C.; Watson, D.C.; Wakarchuk, W.; Campbell, R.; Yaguchi, M.; Jurasek, L.
FEBS Lett. 334, 296-300, 1993
A/Title: Amino acid sequence and thermostability of xylanase A from Schizophyllum commu
A/Reference number: S38973; MUID:94063044; PMID:8243636
A:Accession: S38973
A:Molecule type: protein
A:Residues: 1-197 <OKU>
A/Experimental source: ATCC 38548

C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylonic bonds in xylans
A/Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-197/Domain: endo-1,4-beta-xylanase homology <XYL>
F:87,184/Active site: Glu #status predicted
F:111-160/Disulfide bonds: #status experimental

Query Match 55.5%; Score 586.5; DB 1; Length 197;
Best Local Similarity 56.0%; Pred. No. 4e-38;

Matches 107; Conservative 34; Mismatches 43; Indels 7; Gaps 3;

QY 7 TGVNNGFYFVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXVNFSGS 65
DB 7 TGVNNGFYFVNDHGGVYTTNGPGGQFVSNMNSGPFVKGKMOPTKXVNFSGS 66
QY 66 YNPNGNSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRTQVNPQ 125
DB 67 YNPNGNSYLSYVGMGRNPLIEYIVENFGTNPSTGATKLGVTCDGSVYDIYRTQVNPQ 126
QY 126 PSITGATFYQVSVRRNRSSGVNTACHFNMAOHGLTLGTMDYQIYAVEGY 179
DB 127 PSITGATFYQVSVRRNRSSGVNTACHFNMAOHGLTLGTMDYQIYAVEGY 186
QY 180 FSSGSASITVS 190
DB 187 QSSGTAITITV 197

RESULT 14

JS0590
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 Seconds

(without alignments)
1364.597 Million cell updates/sec

Title: US-09-856-025B-62

Perfect score: 1056
Sequence: 1 QTIQPTGTGNNGYFSYWD.....YQIWAEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	222	1 XYN2_TRIRE	P36217 trichoderma
2	984	93.2	190	1 XYN2_TRIRE	P48793 trichoderma
3	669.5	63.4	225	1 XYN1_EWENI	P55332 aspergillus
4	661.5	62.6	225	1 XYN2_ASPKA	P48883 aspergillus
5	656.5	62.2	225	1 XYN2_ASPKA	O43097 thermomyces
6	655.5	62.1	221	1 XYN2_EWENI	P55333 aspergillus
7	649.5	61.5	225	1 XYN2_ASPNG	P55330 aspergillus
8	642.5	60.8	221	1 XYN1_COCCA	O06562 cochlidiobolus
9	611.5	57.9	227	1 XYN1_HUMIN	P55334 humicola in
10	586.5	55.5	197	1 XYN2_SCHCO	P35809 schizophyllum
11	579	54.8	235	1 XYN2_STRLI	P26515 streptomyces
12	565.5	53.6	233	1 XYN2_MAGGR	P55335 magnaporthe
13	559.5	53.0	644	1 XYN2_CELFI	P54865 cellulomona
14	512	48.5	240	1 XYN2_STRLI	P26220 streptomyces
15	509.5	48.2	210	1 XYN2_BACST	P45705 bacillus st
16	497	47.1	213	1 XYN2_BACST	P18429 bacillus st
17	496	47.0	213	1 XYN2_BACCI	P09850 bacillus ci
18	461	43.7	228	1 XYN2_BACPU	P00694 bacillus pu
19	449.5	42.6	261	1 XYN2_CLOSA	P17127 clostridium
20	436	41.3	512	1 XYN2_CLOSR	P33558 clostridium
21	427.5	40.5	229	1 XYN1_TRIRE	P36218 trichoderma
22	424	40.2	211	1 XYN1_ASPAW	P55338 aspergillus
23	424	40.2	211	1 XYN1_ASPNG	P55339 aspergillus
24	422	40.0	211	1 XYN1_ASPPT	P55331 aspergillus
25	419	39.7	211	1 XYN2_ASPKA	P33557 aspergillus
26	397	37.6	954	1 XYN2_RUMFL	P29126 ruminococcus
27	380.5	36.0	802	1 XYN2_RUMFL	O53317 ruminococcus
28	368.5	34.9	179	1 XYN2_PSEXY	P83513 pseudobuty
29	297	28.1	607	1 XYN2_NEOPA	P29127 neocallimast
30	288.5	27.3	608	1 XYN2_FIBSU	P35811 fibrobacter
31	248	23.5	625	1 XYN2_PIRSP	O12667 pirromyces s
32	100.5	9.5	159	1 GRPA_MEDPA	O09124 medicago fa
33	99	9.4	734	1 PSAB_PINTH	P41640 pinus thunb

ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD;	PRT;	222 AA.
AC	P36217;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (Ec 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanohydrolase 2).				
GN	XYN2.				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreomycetidae; Hypocreales; Hypocreales; Hypocrea.				
OX	NCBI_Taxid=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RX	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkinen N.,				
RA	Harki A., Kubick C.P.,				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biotechnology 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Harki A., Rouvinen J.,				
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.,				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96502263; PubMed=8755744;				
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.,				
RT	"Covalent binding of three epoxalxyl xylosides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CARBOLIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: The N-terminus is blocked.				
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl				
CC	hydrolases).				
CC	-----				
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CC
 DR ENBL, X65573; CAA49293.1; -.
 DR PIR, S39154; S39154.
 DR PDB, 1XJO; 08-AUG-95.
 DR PDB, 1XYP; 08-AUG-95.
 DR PDB, 1ENX; 08-AUG-95.
 DR PDB, 1RED; 11-JAN-97.
 DR PDB, 1RRE; 11-JAN-97.
 DR PDB, 1RRE; 11-JAN-97.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
 KM 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 1 32
 FT ACT_SITE 118 118 ENDO-1,4-BETA-XYLANASE 2.
 FT ACT_SITE 209 209 NUCLEOPHILE.
 FT CARBOHYD 70 70 PROTON DONOR.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT STRAND 34 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT STRAND 38 42
 FT STRAND 43 44
 FT STRAND 45 51
 FT STRAND 57 61
 FT TURN 64 65
 FT TURN 66 71
 FT STRAND 76 83
 FT STRAND 91 101
 FT STRAND 104 113
 FT TURN 114 116
 FT STRAND 117 125
 FT TURN 130 133
 FT STRAND 135 142
 FT TURN 143 144
 FT STRAND 145 157
 FT TURN 160 161
 FT STRAND 164 173
 FT STRAND 180 183
 FT HELIX 184 193
 FT TURN 194 195
 FT STRAND 200 211
 FT STRAND 214 222
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;
 Query Match 97.2%; Score 1026; DB 1; Length 222;
 Best Local Similarity 98.4%; Pred. No. 1.8e-78;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 2
 ID XYN_TRIHA STANDARD; PRT; 190 AA.
 AC P48793;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ENDO-1,4-BETA-XYLANASE (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 DE xylanhydrolase).
 OS Trichoderma harzianum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreales; Hypocreales; Hypocreales.
 OC NCBI_TaxID=5544;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=E58;
 RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
 RA Sadtler J.N.;
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
 RT harzianum E58";
 RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,
 RL Voragen A.G.J. (eds.);
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,
 RA Yaguchi M.;
 RT "High-resolution structures of xylanases from B. circulans and
 RT T. harzianum identify a new folding pattern and implications for the
 RT atomic basis of the catalysis";
 RL (In) Suominen P., Reinikainen T. (eds.);
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,
 RL Foundation for Biotechnical and Industrial Fermentation Research,
 RL Helsinki (1993).
 CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylonicidic
 CC linkages in xylans.
 CC -I- PATHWAY: xylan degradation.
 CC -I- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 DR PDB; 1XND; 20-DEC-94.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; 3D-structure.
 FT ACT_SITE 86 86 NUCLEOPHILE.
 FT ACT_SITE 177 177 PROTON DONOR.
 FT STRAND 3 3
 FT STRAND 6 9
 FT STRAND 14 19
 FT STRAND 25 29
 FT TURN 32 33
 FT STRAND 34 39
 FT STRAND 44 51
 FT TURN 56 57
 FT STRAND 59 69
 FT STRAND 72 81
 FT TURN 82 84
 FT STRAND 85 93
 FT STRAND 98 101
 FT STRAND 103 110
 FT TURN 111 112
 FT STRAND 113 125
 FT TURN 128 129
 FT STRAND 132 141
 FT STRAND 148 151
 FT HELIX 152 161
 FT TURN 162 163
 FT STRAND 168 179

FT	STRAND	182	190	
50	SEQUENCE	190 AA;	20703 MW;	6A0F4D1C3590C698 CRC64;
	Query Match		93.2%;	Score 984; DB 1; Length 190;
	Best Local Similarity		93.7%;	Pred. No. 4,7e-75;
	Matches 178; Conservative		4; Mismatches 8; Indels	0; Gaps 0;
QY	1	QTIGPGTGNNGYFFFSYVNDHGCTATYNTGPGGCFSVVMSNSGNTFVVGGMOPGTRKNKYI	60	
DB	1	QTIGGCTGTSNYYTSSYVNDHGAGCTYNTGGGGSFTVMSNSGNTVAAGKMPGTRKNKYI	60	
QY	61	NFSGSYNPNGNSYLSVYGMSSNPDIIEYIVENFGTNPSTGATKLGEVTCDSVYDIYRT	120	
DB	61	NFSGSYNPNGNSYLSVYGMSSNPDIIEYIVENFGTNPSTGATKLGEVTSDDSVYDIYRT	120	
QY	121	QRVNPSTIIGTATFYQVSVRNHSSGGSVNTAFCEPNAAGHGLTGMDVQVAVEGF	180	
DB	121	QRVNPSTIIGTATFYQVSVRNHSSGGSVNTAFCEPNAAGHGLTGMDVQVAVEGF	180	
QY	181	SSGSASITVS 190		
DB	181	SSGSASITVS 190		
	RESULT 3			
	XYN1_EMENI	STANDARD;	PRT;	225 AA.
ID	XYN1_EMENI	STANDARD;	PRT;	225 AA.
AC	P55332; C00173;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)			
DE	(1,4-beta-D-xylan xylanohydrolase 1).			
OS	Emmerikella nidulans (Aspergillus nidulans).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;			
OC	Eurotiales; Trichocomaceae; Emmentella.			
OX	NCBI_TaxID=162425;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96236210; PubMed=8787417;			
RA	Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;			
RT	"Molecular cloning and expression in Saccharomyces cerevisiae of two			
RT	Aspergillus nidulans xylanase genes.";			
RL	Appl. Environ. Microbiol. 62:2179-2182 (1996).			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic			
CC	linkages in xylans.			
CC	-1- PATHWAY: Xylan degradation.			
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl			
CC	hydrolases).			
CC	-----			
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CC	-----			
DR	EMBL; Z49892; CAA90073.1; -.			
DR	PIR; S57477; S57477.			
DR	HSSP; P48793; 1XND.			
DR	InterPro; IPR008985; Cma_1like_1ec.g1.			
DR	InterPro; IPR001137; Glyco_hydro_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLHYDRLAS11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Xylan degradation; Hydrolase; Glycosidase; signal.			
FT	CHAIN	1		
FT	CHAIN	19		
FT	ACET SITE	20		
FT	ACET SITE	121		
FT	ACET SITE	212		
FT	SEQUENCE	225 AA;		

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Query Match Similarity      63.4%; Score 669.5; DB 1; Length 225;
Best Local Similarity     65.0%; Pred. No. 7,8e-49;
Matches    119; Conservative   25; Mismatches   38; Indels    1; Gaps    1

QY      7 TGVANGVYYSYWNGDHGGVYTTNPGFGGSPSVNMSGSGNFVGKMGQPCTKANVTINPSGSY 66
DB      43 TGWSNGYYYSPMTGGCGDVITYTNGAGGSGYTIVQWSNVGNFVGKGMPPS-TRTINYGGSF 101
QY      67 NPNGSYSYVYGSMRNPLEIYYIVNFCFTVPNSTGATLGEVTCDSGYVDIYTORVANP 126
DB      102 NPSNGXYLAIVGWTONPLIEIYYIVESYGTITNPGSGGQRGVISYGATIIDYTAIRYNAP 161
QY      127 SIIGTATPYQYWVSVRNRHSSGSVNTACHFNAMAQHGLTLGMDYOIVAEGVFSSGSAS 186
DB      162 SIEGTATPEQEWVSYSQSKETGTGTVTTANHFAMALAKRLTGTHNYQIVATEGYQGSSGSAS 221
QY      187 ITV 189
DB      222 ITV 224

RESULT 4
XNB ASPKA
ID_XNB ASPKA STANDARD; PRT; 225 AA.
AC_P48824:
DN 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (BC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XYNB.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi)..
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4308;
RA Ito K.;
RU Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC -1- CATALYTIC ACTIVITY: Endo-hydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC -----
CC EMBL; D38070; BA007264.1; -.
CC HSSP; P36217; IXO.
DR InterPro; IPRO08985; Cons_like_1ec_g1.
DR InterPro; IPRO01137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00311; GLHYDRLA5E11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR Xylan degradation; Hydroxylase; Glycosidase; Signal.
KM SIGNAL
FT CHAIN 1
FT SIGNAL 18
FT FT 19 POTENTIAL.
FT ACT SITE 121 ENDO-1,4-BETA-XYLANASE B.
FT ACT SITE 121 NUCEOPHILE (BY SIMILARITY).
FT ACT SITE 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match Similarity      62.6%; Score 661.5; DB 1; Length 225;
Best Local Similarity     65.0%; Pred. No. 3,6e-48;
Matches    119; Conservative   23; Mismatches   40; Indels    1; Gaps    1;

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OY 7 TGVNNGFYFSGVNDHGSGVTYTNPGGQFSPVMSNSGNFVGGKGNQPGTKNRYINPSGSV 66
DB 43 TGVNNGFYFSGVNDHGSGVTYTNPGGQFSPVMSNSGNFVGGKGNQPGTKNRYINPSGSV 101
OY 67 NPNNGNSYLSYSGSRNPLIEYIVENFGTYNPGTGATLGEVYCDSDSVYDIYETQFVNQF 126
DB 102 TPGSNGSLSYGWTTPDLIETIVESYGDYINPGSGGTTGKGNVSDSDSVYDIYATATNAP 161
OY 127 SIIGTATFYQVYSVRNRNRSNGSVNTACFNMAQHGTLTGMDYQIVAVEGTFSSGSAS 186
DB 162 SIIGTATFYQVYSVRNRNRSNGSVNTACFNMAQHGTLTGMDYQIVAVEGTFSSGSAS 221
OY 187 ITV 189
DB 222 ITV 224

RESULT 5
XVNA THELA STANDARD; PRT; 225 AA.
AC 043057;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
  xylan xylanohydrolase).
GN XVNA.
OS Thermomyces lanuginosus (Fusicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
CX NCBI_TaxID=5541;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=8879171;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT Cloning and characterization of the gene for the thermostable
  xylanase Xvna from Thermomyces lanuginosus."
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=98426042; PubMed=9753433;
RA Gruber K., Klinsch G., Hayn M., Schlacher A., Steiner W.,
  Katky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution
  X-ray structure and modeling studies."
RL Biochemistry 37:13475-13485(1998).
CC -1- FUNCTION: THERMOSTABLE XYLANASE.
CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic
  linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
  hydrolases).
CC -----
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  CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; U35436; AAB94633.1; -
DB PDB; 1YNA; 12-FEB-97;
DB InterPro; IPR008985; ConA_like_1ec_g1.
DB InterPro; IPR001137; Glyco_hydro_11.
DB Pfam; PF00457; Glyco_hydro_11; 1.
DB PRINTS; PR00911; GLYCDRLASE1.
DB PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DB PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DB Xylan degradation; Xylanase; Glycosidase; Signal; 3D-structure;
  KM Pyroliidone carboxylic acid.

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FT SIGNAL 1 31
FT CHAIN 32 225
FT ACT_SITE 117 117
FT ACT_SITE 209 209
FT MOD_RES 32 32
FT DISULFID 141 185
FT STRAND 33 33
FT STRAND 37 41
FT TURN 42 43
FT STRAND 44 50
FT STRAND 46 60
FT TURN 63 64
FT TURN 65 70
FT STRAND 75 82
FT STRAND 90 100
FT STRAND 103 112
FT TURN 113 115
FT STRAND 116 124
FT TURN 129 132
FT STRAND 134 141
FT TURN 142 143
FT STRAND 144 158
FT TURN 159 160
FT STRAND 161 172
FT STRAND 179 182
FT HELIX 183 192
FT TURN 193 194
FT STRAND 200 211
FT STRAND 214 223
SQ SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 62.2%; Score 656.5; DB 1; Length 225;
Best Local Similarity 61.3%; Pred. No. 9.4e-48;
Matches 117; Conservative 28; Mismatches 45; Indels 1; Gaps 1;

OY 1 QTIQGTGYNNGFYFSGVNDHGSGVTYTNPGGQFSPVMSNSGNFVGGKGNQPGTKNRYI 60
DB 32 QTPNSEGMDHGYYSWMSDGAQATYTNLEGTYEISMWDGKXLVGGKGNPGLNARAI 91
OY 61 NFSGSYNNGNSYLSYVGSNRNPLIEYIVENFGTYNPGTGATLGEVYCDSDSVYDIYRT 120
DB 92 HREGYQNGNSYLAIVGWTNPLVEYIVENFGTYNPGTGATLGEVYCDSDSVYDIYRT 151
OY 121 GVNQPSIIGTATFYQVYSVRNRNRSNGSVNTACFNMAQHGTLTGMDYQIVAVEGY 179
DB 152 TRVNPISDGTCTPQVYSVRNQRKTSQVGTGCHFDMAAGLVNNGDHYQIVAVEGY 211
OY 180 FSSGSASITVS 190
DB 212 FSSGYARITVA 222

RESULT 6
ID XVNA2_EMENT STANDARD; PRT; 221 AA.
AC P55333; Q00176;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
DB (1,4-beta-D-xylan xylanohydrolase 2).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
  OC Eurotiaceae; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96736210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
  RT Aspergillus nidulans xylanase genes."
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolasis of 1,4-beta-D-xylosidic

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CC      linkages in xylans.
CC      -1- PATHWAY: Xylan degradation.
CC      -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC      hydrolases).
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Z49893; CAA0074.1; -.
DR      PIR; S57469; S57469.
DR      HSBP; P48793; IXND.
DR      InterPro; IPR008985; ConA_like_1ec_g1.
DR      InterPro; IPR001137; Glyco_hydro_11.
DR      Pfam; PF00457; Glyco_hydro_11; 1.
DR      PRINTS; PR00911; GLHYDRLASE11.
DR      PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR      Kxlan degradation; Hydrolase; Glycosidase; Signal.
FT      SIGNAL 1
FT      CHAIN 19 221
FT      ACT_SITE 117 117 ENDO-1,4-BETA-XYLANASE 2.
FT      ACT_SITE 208 208 NUCLEOPHILE (BY SIMILARITY).
FT      ACT_SITE 208 208 PROTON DONOR (BY SIMILARITY).
SQ      SEQUENCE 221 AA; 23517 MW; 42665E80DDE9475 CRC64;

Query Match 62.1%; Score 655.5; DB 1; Length 221;
Best Local Similarity 64.7%; Pred. No. 1,1e-47;
Matches 119; Conservative 26; Mismatches 38; Indels 1; Gaps 1;

QY 7 TGVNNGFYFYSYMNNDGCVTYTNGPGQGFVSVMNSNGFVGKGMQPGTKNKNVINFSGSY 66
DB 39 TGTSGFYYSFMTDGGDVTYTNGDGSYVEMTKVNFVGKGMNNGS-SQTLISVSGSF 97
QY 67 NPNGNSYLSVYGSNRNPLIEYIVENFGTYNPGTATKLGKGLGVCYVDIYRTORVNP 126
DB 98 IPSGNGYLSVYGMNQPLIEYIVESYGDYNPAGTHGGLSDGSTYDIYATENAP 157
QY 127 SIIGTATFYQYWSVRNRHSSGSVNTACHFNMAAOHGLTGMDYQIVAVEGTFSSGSAS 186
DB 158 SIIGTATFYQYWSVRNRHSSGSVNTACHFNMAAOHGLTGMDYQIVAVEGTFSSGSAS 217
QY 187 ITVS 190
DB 218 ITVS 221

RESULT 7
XN2 ASPNG STANDARD; PRT; 225 AA.
AC P55330; O12557;
DT 01-FEB-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_Taxid=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloridic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

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CC      hydrolases).
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; D38071; BAA07265.1; -.
DR      HSBP; P09850; IXNB.
DR      InterPro; IPR008985; ConA_like_1ec_g1.
DR      InterPro; IPR001137; Glyco_hydro_11.
DR      Pfam; PF00457; Glyco_hydro_11; 1.
DR      PRINTS; PR00911; GLHYDRLASE11.
DR      PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR      PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR      Kxlan degradation; Hydrolase; Glycosidase; Signal.
FT      PROPEP 1 37
FT      CHAIN 38 225
FT      ACT_SITE 121 121 ENDO-1,4-BETA-XYLANASE II.
FT      ACT_SITE 212 212 NUCLEOPHILE (BY SIMILARITY).
FT      ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ      SEQUENCE 225 AA; 24057 MW; C4B8B007AB288FD CRC64;

Query Match 61.5%; Score 649.5; DB 1; Length 225;
Best Local Similarity 64.5%; Pred. No. 3.6e-47;
Matches 118; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

QY 7 TGVNNGFYFYSYMNNDGCVTYTNGPGQGFVSVMNSNGFVGKGMQPGTKNKNVINFSGSY 66
DB 43 TGVNNGFYFYSFMTDGGDVTYTNGDGSYVEMTKVNFVGKGMNNGS-SQTLISVSGSF 101
QY 67 NPNGNSYLSVYGSNRNPLIEYIVENFGTYNPGTATKLGKGLGVCYVDIYRTORVNP 126
DB 102 TPGSGYLSVYGMNQPLIEYIVESYGDYNPAGTHGGLSDGSTYDIYATENAP 161
QY 127 SIIGTATFYQYWSVRNRHSSGSVNTACHFNMAAOHGLTGMDYQIVAVEGTFSSGSAS 186
DB 162 SIIGTATFYQYWSVRNRHSSGSVNTACHFNMAAOHGLTGMDYQIVAVEGTFSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 8
XN1 COCCA STANDARD; PRT; 221 AA.
AC O06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_Taxid=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RC MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RL gene from the maize pathogen Cochliobolus carbonum.";
RN Mol. Plant Microbe Interact. 6:467-473 (1993).
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";

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Physiol. Mol. Plant Pathol. 40:39-47(1992).
 CC -1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
 CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
 CC WALLS.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PIM: The N-terminus is blocked.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L13596; AAA33024.1; -.
 CC HSSP: O43097; 1YNA.
 CC InterPro: IPR008985; Cons. like lec.g1.
 CC InterPro: IPR001137; Glyco_hydro.11.
 CC Pfam: PF00457; Glyco_hydro.11; 1.
 CC PRINTS: PR00911; GLYHDLASE1.
 CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
 CC Xylan degradation; Hydrolase; Glycosidase; Signal.
 KW SIGNAL 1 30
 FT CHAIN 1 221
 FT ACT_SITE 115 221
 FT ACT_SITE 206 221
 FT CONFLICT 81 206
 FT CONFLICT 107 107
 FT CONFLICT 131 131
 FT SEQUENCE 221 AA; 23728 MW; 59DBD983FCB08C CRC64;
 SQ
 Query Match 60.8%; Score 642.5; DB 1; Length 221;
 Best Local Similarity 61.6%; Pred. No. 1.3e-46;
 Matches 117; Conservative 25; Mismatches 47; Indels 1; Gaps 1;
 QY 1 QTIQPTGVNNGSYVSYNDGAGVTYTNPGCGFSVWNSGQFVGGKMGQPGTKXKVI 60
 DB 31 QNTNGECTHNGCWSWSDGCAATYTNAGSGSYVSWGSGNLVGGKMNNGTA-RTI 89
 QY 61 NFGSGYNPNNGSYLVYSGWNRNPLIEYIVENFGTYNPGTATKLGVTCDGSYDIYRT 120
 DB 90 TYSGTYYNNGSYLVAVGWTNPLVEYIVENFGTYNPGTATKLGVTCDGSYDIYRT 149
 QY 121 QVWNPSTIGATFYQWVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQVAVEGYF 180
 DB 150 TRNOPSTIDGTRTQQTWSTVQRKSSGSVNMKTHFDAMASKGNLQGHYYQIVATGCTF 209
 QY 181 SSGSASITVS 190
 DB 210 STGNQITVN 219
 RESULT 9
 XYN1 HUMIN STANDARD; PRT; 227 AA.
 AC P55334; Q12625;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 DE (1,4-Beta-D-Xylan xylanohydrolase 1).
 GN XYL1.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=94247364; PubMed=8190078;
 RA Dalboege H., Hansen H.P.H.;
 RT "A novel method for efficient expression cloning of fungal enzyme
 RT genes";
 RL Mol. Genet. 243:253-260(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL: X76047; CAA53632.1; -.
 CC PIR: S43919; S43919.
 CC HSSP: O43097; 1YNA.
 CC InterPro: IPR008985; Cons. like lec.g1.
 CC InterPro: IPR001137; Glyco_hydro.11.
 CC Pfam: PF00457; Glyco_hydro.11; 1.
 CC PRINTS: PR00911; GLYHDLASE1.
 CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11.2; 1.
 CC Xylan degradation; Hydrolase; Glycosidase; Signal.
 KW SIGNAL 1 19
 FT CHAIN 1 227
 FT ACT_SITE 121 227
 FT ACT_SITE 212 212
 FT ACT_SITE 227 227
 FT SEQUENCE 227 AA; 25601 MW; 5C2F6ADCFEADAF CRC64;
 SQ
 Query Match 57.9%; Score 611.5; DB 1; Length 227;
 Best Local Similarity 58.8%; Pred. No. 5.2e-44;
 Matches 107; Conservative 25; Mismatches 49; Indels 1; Gaps 1;
 QY 8 GYNNGYFYSYNDGAGVTYTNPGCGFSVWNSGQFVGGKMGQPGTKXKVINFFSSYN 67
 DB 44 GHNHNYFYSWSDGGQVQYTNLBSRYQVNRNNGFVGGKMNNGTA-RTIYGGYFN 102
 QY 68 PNGNSYLVYSGWNRNPLIEYIVENFGTYNPGTATKLGVTCDGSYDIYRTQVNPQS 127
 DB 103 PGNNGYLVAVGWTNPLVEYIVENFGTYNPGTATKLGVTCDGSYDIYRTQVNPQS 162
 QY 128 ITGRTFYQVWVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQVAVEGYF 187
 DB 163 IDGTRTFQOYVSRNRHSSGSVNTACHFNAMAQHGTLTGTMDOYQVAVEGYF 222
 QY 188 TV 189
 DB 223 YV 224
 RESULT 10
 XYN1 SCHCO STANDARD; PRT; 197 AA.
 AC P35809;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-Xylan
 DE xylanohydrolase A).
 GN XYN1.
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 SEQUENCE.

RC STRAIN=ATCC 38548 / Delmar;
 RA Yaguchi M., Roy C., Ujite M., Watson D.C., Wakarchuk W.,
 RL (In) Vissers J., Beldman G., Kusters-van Someren M.A.,
 RL Voragen A.G.J. (eds.);
 RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
 RN (2)
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC STRAIN=ATCC 38548 / Delmar;
 RX MEDLINE=94063044; PubMed=8243636;
 RA Oku T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
 RA Urassek L., Paice M.G.;
 RT "Amino acid sequence and thermostability of xylanase A from
 RT Schizophyllum commune.";
 RL FEBS Lett. 334:296-300(1993).
 RN (3)
 RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
 RC STRAIN=ATCC 38548 / Delmar;
 RX MEDLINE=94158888; PubMed=7906649;
 RA Bray M.R., Clarke A.J.;
 RT "Identification of a glutamate residue at the active site of xylanase
 RT A from Schizophyllum commune.";
 RL Eur. J. Biochem. 219:821-827(1994).
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
 CC xylanase has a very broad pH activity.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 DR PIR: A44597; A44597.
 DR HSSP: O43097; 1XNA.
 DR InterPro: IPR008985; Cons. like lec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase.
 FT ACT_SITE 87
 FT ACT_SITE 87 NUCLEOPHILE (PROBABLE)
 FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 111 160
 SQ SEQUENCE 197 AA; 20978 MW; 42C8074B67C1FBE9 CRC64;
 Query Match 55.5%; Score 586.5; DB 1; Length 197;
 Best Local Similarity 56.0%; Pred. No. 5.3e-42;
 Matches 107; Conservative 34; Mismatches 43; Indels 7; Gaps 3;

DE (1,4-beta-D-xylan xylanhidrolase B).
 GN XLNB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxId=1916;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
 RC STRAIN=66 / 1326;
 RX MEDLINE=92077439; PubMed=1743521;
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.,
 RT "Sequences of three genes specifying xylanases in Streptomyces
 RT lividans.";
 RL Gene 107:75-82(1991).
 RN (2)
 RP REVISIONS TO 29-32 AND 252-307.
 RC STRAIN=66 / 1326;
 RX MEDLINE=95189090; PubMed=7533741;
 RA Shareck F., Beely P., Morosoli R., Kluepfel D.,
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
 RT reveals genes encoding acetyl xylan esterase and the RNA component of
 RT ribonuclease P.";
 RL Gene 153:105-109(1995).
 RN (3)
 RP REVISION TO 225.
 RA Shareck F.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
 CC component of plant cell-walls. XLNA and XLNB seem to act
 CC sequentially on the substrate to yield xylobiose and xylose
 CC as carbon sources.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: M64552; AAC06114.2; -.
 DR HSSP: P09850; 1XNB.
 DR InterPro: IPR001919; Bac_cellose-bind.
 DR InterPro: IPR008985; Cellul bind.
 DR InterPro: IPR008985; Cons. like lec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDLASE11.
 DR SMART: SMO0637; CBD_11; 1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 41
 FT CHAIN 42 335
 FT DOMAIN 42 230
 FT DOMAIN 231 249
 FT DOMAIN 250 335
 FT ACT_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 335 AA; 35575 MW; 513B145B8BF0CC CRC64;
 Query Match 54.8%; Score 579; DB 1; Length 335;
 Best Local Similarity 54.0%; Pred. No. 4.1e-41;
 Matches 107; Conservative 32; Mismatches 43; Indels 16; Gaps 5;

Db 36 PGTAADTVTTTNOEGTNNNGYYSFWTDSQIVSNMNGSGGXYSTSMRNTGNFVACKGNA 95
 QY 53 PGRKXKYNFSGSNPNPNSYLSVYGSNRPLIEYIVENFGTYNPGSTGATKLGVEYTCOG 112
 Db 96 NGGR-RVQYSGSFNPGNAYLALYGTSTNPVLEYIIVDNWGYRR-TGEYK-GYTTSDG 152
 QY 113 SYVDIYFQGVNPSIIIGTATFYQWVSRNHRSSGVSNTACHFNMAOGLTLGTM-D-Y 171
 Db 153 GTVDIYKTRTVNKPVSVEGTRTFQYWSVRSKRTGTGTTGNHFDAMAGMPLGNFSYX 212
 QY 172 QIVAVEGPFSSGASITV 189
 Db 213 MIMATSGYSSGSSINW 230

RESULT 12

XYN2_MAGR STANDARD; PRT; 233 AA.

AC P5335; 001171; Created
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
 GN XYN2
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KEN60-19;
 RX MEDLINE=96172742; PubMed=8589407;
 RA Wu S.C., Kautman S., Darvill A.G., Alberstein P.,
 RT "Purification, cloning and characterization of two xylanases from
 RT Magnaporthe grisea, the rice blast fungus."
 RL Mol. Plant Microbe Interact. 8:506-514(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL; J37529; AAC41683.1; -
 DR HSSP; O43097; YNA.
 DR InterPro; IPR008985; ConA_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASB11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM xylan degradation; Hydrolyase; Glycosidase; Signal.
 FT SIGNAL
 FT CHAIN 1 39
 FT ACT SITE 40 233 ENDO-1,4-BETA-XYLANSASE 22.
 FT ACT SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 217 217 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;

Query Match 53.6%; Score 565.5; DB 1; Length 233;
 Best Local Similarity 51.8%; Pred. No. 3.6e-40;
 Matches 99; Conservative 34; Mismatches 55; Indels 3; Gaps 2;

QY 1 OTIOPGTYNNGYYSYVNDHGQVYTYNGFGQFVYWNSSGNFVCGKMGQPTGXKVI 60
 Db 40 QSTGSTRHNGHYYSYVNDHGQVYTYNGFGQFVYWNSSGNFVCGKMGQPTGXKVI 98

QY 61 NFGSSYNP--NGNSYLSVYGSNRPLIEYIVENFGTYNPGSTGATKLGVEYTCOGSVYDIY 118
 Db 99 TYSGTFNPNVNNGNAYLCLYGTQNPVLEYIILEYVNGYNSGNSQSGTLQAAAGTYTLH 158
 QY 119 RTQVNOPPSIIIGTATFYQWVSRNHRSSGVSNTACHFNMAOGLTLGTM-DQIVAVEG 178
 Db 159 ESTRVNDSIGCTTFQYVMAIROKNSGVINIGERFQWERAQMGNGHNTVATLEG 218
 QY 179 YFSSGASITV 189
 Db 219 YRSAGNSINW 229

RESULT 13

XYND_CELFI STANDARD; PRT; 644 AA.

AC P54865;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
 GN XYND
 OS Cellulomonas fimi.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcales; Cellulomonadaceae; Cellulomonas.
 OX NCBI_TaxID=1708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=221;
 RX MEDLINE=94224155; PubMed=8170399;
 RA Milward-Sadler S.J., Poole D.M., Henriksat B., Hazlewood G.P.,
 RA Clarke J.H., Gilbert H.J.;
 RT "Evidence for a general role for high-affinity non-catalytic
 RT cellulose binding domains in microbial plant cell wall hydrolyses."
 RL Mol. Microbiol. 11:375-382(1994).
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable
 CC activity against polysaccharides other than xylan. Hydrolyses
 CC glucosidic bonds with retention of anomeric configuration.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL; X76729; CAA54145.1; -
 DR PIR; I40712; I40712.
 DR PDB; 1EBB; 25-MAY-01.
 DR PDB; 1ESC; 25-MAY-01.
 DR PDB; 1HEH; 10-MAY-01.
 DR PDB; 1HEJ; 10-MAY-01.
 DR PDB; 1XBD; 21-JUL-99.
 DR PDB; 2XBD; 21-JUL-99.
 DR InterPro; IPR001919; Bac_celose-bind.
 DR InterPro; IPR008965; Cellul bind.
 DR InterPro; IPR008985; ConA_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR InterPro; IPR002509; Polysac_deacet.
 DR Pfam; PF00553; CBM 2; 2.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR Pfam; PR01522; Polysac_deacet; 1.
 DR PRINTS; PR00911; GLHYDRLASB11.
 DR SMART; SM00637; CBD_1; 2.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

DR 1 OTIOPGTYNNGYYSYVNDHGQVYTYNGFGQFVYWNSSGNFVCGKMGQPTGXKVI 60
 DR 40 QSTGSTRHNGHYYSYVNDHGQVYTYNGFGQFVYWNSSGNFVCGKMGQPTGXKVI 98

KM Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat;
 3D-structure. 1
 FT SIGNAL 43
 FT CHAIN 44 644
 FT DOMAIN 44 230
 FT DOMAIN 231 245
 FT DOMAIN 246 644
 FT REPEAT 246 333
 FT REPEAT 557 644
 FT DOMAIN 337 350
 FT DOMAIN 548 556
 FT DOMAIN 231 238
 FT DOMAIN 241 245
 FT DOMAIN 548 558
 FT ACT_SITE 126 126
 FT ACT_SITE 216 216
 SQ SEQUENCE 644 AA; 66581 MW; 568045CC6DE1820 CRC64;
 Query Match 53.0%; Score 559.5; DB 1; Length 644;
 Best Local Similarity 54.6%; Pred. No. 3.5e-39;
 Matches 101; Conservative 38; Mismatches 41; Indels 5; Gaps 4;
 QY 7 TGNNNGFYFYVNDHGCVTYTNGPGQGFVSNMNSGNFVGGKMGQPGTKNKNVNFSGSY 66
 DB 49 TGTHDGYFYSFMTDPSGSVSDNLNNGGGYR-RMSNTGNFVAGKMGWSTGGR-KTVSYSGQF 106
 QY NPNNGNSLYVYGSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVVDIYRTORNOP 126
 DB 107 NPSNAILITLXGWTQSPLEVIYIVDSWGTIRPT--GTFMGVITSDGTYIYIRQYNKE 164
 QY 127 SIIG-TATFYQYMSVRNRHRSRGS-VNTACHFNMAOHGLTGMVDYOIVAVEGYFSSGA 185
 DB 165 SIEDSSSTFYQYMSVVRQKRTGTTTGNHFDAMASKMNLGRHNMVIMATEGYQSSGS 224
 QY 186 SITVS 190
 DB 225 SITVS 229
 RESULT 14
 XYNL STRLI
 ID XYNL STRLI STANDARD; PRT; 240 AA.
 AC P26220;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
 DE (1,4-beta-D-xylan xylanohydrolase C).
 GN XINC.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
 RC STRAIN=66 / 1326;
 RA MEDLINE=82077439; PubMed=1743521;
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.,
 RT "Sequences of three genes specifying xylanases in Streptomyces
 lividans."
 RL Gene 107:75-82(1991).
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
 CC component of plant cell-walls.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family 6 (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL; M64553; AAA26836.1; -
 CC EMBL; A25307; CA01768.1; -
 CC FIR; J80591; J80591.
 CC HSSP; P09850; 1XNB.
 CC InterPro; IPRO08985; Cona_1like_1ec_g1.
 CC InterPro; IPRO01137; Glyco_hydro_11.
 CC InterPro; IPRO06311; Tat.
 CC Pfam; PF00457; Glyco_hydro_11; 1.
 CC PRINTS; PRO0911; GHYDRLASE1.
 CC TIGRfam; TIGR01409; Tat_signal_seq; 1.
 CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 49
 FT CHAIN 50 240
 FT ACT_SITE 134 134
 FT ACT_SITE 226 226
 SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;
 Query Match 48.5%; Score 512; DB 1; Length 240;
 Best Local Similarity 52.1%; Pred. No. 1e-35;
 Matches 100; Conservative 30; Mismatches 52; Indels 10; Gaps 6;
 QY 2 TIQGTGNNNGFYFYVNDHGCVTYTNGPGQGFVSNMNSGNFVGGKMGQPGTKNKNV 61
 DB 55 TIQGTGNNNGFYFYVNDHGCVTYTNGPGQGFVSNMNSGNFVGGKMGQPGTKNKNV 109
 QY 62 FSGSYNPNNSLYVYGSRNPLIEYIVENFGTNPSTGATKLGCVTCDGSVVDIYRTORNOP 121
 DB 110 YNGYFNPNNGYGCIXGWTNSPLVEYIVDSWGTIRPT--GTYRK-GTVSSDGTIYIYRT 167
 QY 122 RVNQPSTIGTATFYQYMSVRNRHRSRGS--VNTACHFNMAOHGLTGMVDYOIVAVEG 178
 DB 168 RYNAPSVEGTKTFFQYMSVVRQKRTGTTTGNHFDAMARAGNMQFRYYMIMATEG 227
 QY 179 YFSSGSASTVS 190
 DB 228 YQSSGSSTIVS 239
 RESULT 15
 XYNL BACST
 ID XYNL BACST STANDARD; PRT; 210 AA.
 AC P45705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 DE (1,4-beta-D-xylan xylanohydrolase A).
 GN XYNL.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=No. 236;
 RA Cho S., Choi Y.,
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
 RT Bacillus stearothermophilus."
 RL J. Microbiol. Biotechnol. 5:117-124(1995).
 CC [2]
 CC REVISIONS.
 CC RC STRAIN=No. 236;
 CC RA Cho S., Choi Y.;
 CC Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.

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CC -! SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
CC EMBL; U15985; AAB72117.1; -.
CC HSSP; P03850; 1XNB.
CC InterPro; IPR008985; Cons. like lec.g1.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHDBLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC SIGNAL 1 19
CC CHAIN 20 210
CC ACT_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).
CC ACT_SITE 197 197 PROTON DONOR (BY SIMILARITY).
CC SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 48.2%; Score 509.5; DB 1; Length 210;
Best Local Similarity 53.0%; Pred. No. 1,4e-35;
Matches 96; Conservative 30; Mismatches 48; Indels 7; Gaps 5;

QY 14 FYSTWNDGHGVTYTNNGPGQFSYWNMSNGNFVGKQKMGPGTKNKVINF-SGSYNPNQNS 72
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
31 YMOYMTDGGGMVNAVNPGGNYSVTWONTGNFVVGKMTVGSPPRVNINAGIWEPSGNG 90

QY 73 YLSTVYGSRNPLIEYIVENFGTYNPSTGATKLGVTCDGQSVYDIYNTQCRVNPQSIIGTA 132
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
91 YLTIXGKTRNALIETYYVDMSGTYRP-TGNVYK-GTVNSDGGTYDIYTTMKRYNAPSIDGTQ 148

QY 133 TFQYVMSVRNRHSSG--SVNTACHPNANAQHGCLTIG-TMDYQIVAVEGEYSSGSASIT 188
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
149 TFQGFMSVRQSKRPTGSNVSITFSNHNAMRSKGMNIGSSMAYOVLALEGYQSSGRSNVT 208

QY 189 V 189
Db 209 V 209

```

Search completed: June 30, 2004, 19:40:09
 Job time : 8.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds
(without alignments)
1816.620 Million cell updates/sec

Title: US-09-856-025B-62
Perfect score: 1056
Sequence: 1 QTIQPGTGNNGYFYSYWN.....YQIVAVEGYRSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_muc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1026	97.2	223	Q02244	trichoderma
2	1014	96.0	223	Q09015	trichoderma
3	922	87.3	223	Q728Q3	trichoderma
4	898	85.0	220	Q8J0T4	trichoderma
5	869	82.3	223	Q9HEV9	trichoderma
6	764.5	72.4	241	Q12580	chaetomium
7	742.5	70.3	293	Q871E8	neurospora
8	709.5	67.2	261	Q8J1V6	chaetomium
9	703.5	66.6	219	Q12579	chaetomium
10	690.5	65.4	232	Q8HPA4	aspergillus
11	686.5	65.0	295	Q8CIR2	fusarium ox
12	681.5	64.5	290	Q9HEZ0	phanerochaete
13	676.5	64.5	227	Q00263	ascospora
14	670.5	63.5	227	Q8UV33	setosphaeria
15	670.5	63.5	225	Q8TG22	aspergillus
16	650.5	61.6	225	Q8TG22	aspergillus

17	644.5	61.0	194	3	P81536	paecilomyces
18	641	60.7	221	3	Q9WUQ2	penicillium
19	640.5	60.7	230	3	Q8J1V5	chaetomium
20	632.5	59.9	226	3	Q9HPH0	penicillium
21	629.5	59.6	243	3	Q8VUT4	pseudomonas
22	627.5	59.4	231	3	Q13447	cochliobolus
23	620.5	58.8	231	3	Q00350	cochliobolus
24	614.5	58.2	221	3	P87037	aspergillus
25	612.5	58.0	227	3	Q9HGE1	humicola
26	604.5	57.2	231	3	Q7ZAS7	glibberella
27	604.5	57.2	338	2	Q56265	thermonos
28	603.5	57.1	335	2	Q08346	streptomyces
29	603.5	57.1	335	2	Q9RMM4	streptomyces
30	602.5	57.1	335	2	Q9RQ88	promicromonas
31	600.5	56.9	231	3	Q9C1R1	fusarium ox
32	598.5	56.7	283	3	Q96UV7	lentisphaeria
33	596	56.4	216	3	Q74716	claviceps
34	587	55.6	228	2	Q59962	streptomyces
35	584.5	55.4	344	2	Q8GMV7	nonomuraea
36	578.5	54.8	329	2	Q9RMM9	streptomyces
37	576	54.5	335	16	Q9RXK6	streptomyces
38	556	52.7	191	2	Q9EM89	caldicellul
39	523.5	49.6	361	2	Q52375	dictyogloma
40	520.5	49.3	360	2	P77853	pseudomonas
41	520.5	49.3	661	2	Q59674	uncultured
42	516	48.9	352	2	Q84DD2	uncultured
43	515.5	48.8	241	16	Q9R172	streptomyces
44	510.5	48.3	656	2	Q59300	cellvibrio
45	510	48.3	240	2	Q56013	streptomyces

ALIGNMENTS

RESULT 1

ID Q02244 PRELIMINARY; PRT; 223 AA.

AC Q02244;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Endoxylanase II (EC 3.2.1.6) (Endo-1,4-beta-xylanase).

GN XLN2.
OS Trichoderma reesei (Hypocreales; Sordariomycetes).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=94088442; PubMed=8264524;
RA Saaralahti R., Palonen M., Fagerstrom R., Suominen P.L.,
Nevalainen K.M.;

RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei
endoxylanase II (PI 9) gene xln2.";
RL Mol. Gen. Genet. 241:497-503 (1993).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
LINKAGES IN XYLANS.

CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
HYDROLASES).

EMBL: S67387; AAB29346.1; -.
CC DR EIR: S39883; S39883.
DR HSSP: P36217; 1XVO.
DR GO: GO:0004553; Fungal hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; Polysaccharide metabolic process; IEA.
DR InterPro: IPR008985; Cons. like_1ec.g1.
DR InterPro: IPR01137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GHYDRASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00778; Xylan degradation.
KW Glycosidase; Hydrolase; Xylan degradation.

Q02244 223 AA; 24069 MW; 79668149EADA22F9 CRC64;
SQ

Query Match 97.2%; Score 1026; DB 3; Length 223;
 Best Local Similarity 98.4%; Pred. No. 3.7e-71;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 60
 Db 34 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 93

Qy 61 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 Db 94 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

Qy 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNAMAQGLTGTMDYQIVAVEGYF 180
 Db 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANHFANMAQGLTGTMDYQIVAVEGYF 213

Qy 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 2

Qy 099015 PRELIMINARY; PRT; 223 AA.
 AC 099015;
 RC 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYN2.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 CX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=QM 6a;
 RA MEDLINE=97076932; PubMed=8975597;
 RA la Grange D.C., Pretorius I.S., Van Zyl W.H.;
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
 RT Saccharomyces cerevisiae";
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).
 CC -1- CATALYTIC ACTIVITY: ENDODIHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; U24191; AA850278.1; -.
 DR HSEF; P36217; IXYO.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR GlycoStase; Hydrolyase; Signal; Xylan degradation.
 FM SIGNAL 1 33 POTENTIAL.
 FT CHAIN 34 223 BETA-XYLANASE.
 FT CHAIN 34 223 BETA-XYLANASE.
 SQ SEQUENCE 223 AA; 23981 MW; F696B545DAC0EB4 CRC64;

Query Match 96.0%; Score 1014; DB 3; Length 223;
 Best Local Similarity 97.4%; Pred. No. 3.1e-70;
 Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 60
 Db 34 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 93

Qy 61 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120

Db 94 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

Qy 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNAMAQGLTGTMDYQIVAVEGYF 180
 Db 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANHFANMAQGLTGTMDYQIVAVEGYF 213

Qy 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 3

Qy 072803 PRELIMINARY; PRT; 223 AA.
 AC 072803;
 RC 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
 OS Trichoderma viride.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 CX NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YNCC0183;
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,
 RA Yang Z.W.;
 RT "Cloning and characterization of endo-1,4-beta-xylanase from
 RT Trichoderma viride YNCC0183";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY320046; AAP83925.1; -.
 CC Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4E76FA03CAE CRC64;

Query Match 87.3%; Score 922; DB 3; Length 223;
 Best Local Similarity 86.3%; Pred. No. 3.5e-63;
 Matches 164; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 60
 Db 34 QTIPTGTGYNNGSYVSWNDGCGVTTNPGCGQFSVWNSGNGFVGKGMQPGTKXKVI 93

Qy 61 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 Db 94 NFSGSYNPNNGNSYLSVYGSWRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153

Qy 121 QRVNPSIIGTATFYQYWSVRNRSSGSVNTACHFNAMAQGLTGTMDYQIVAVEGYF 180
 Db 154 QRVNPSIIGTATFYQYWSVRNRSSGSVNTANHFANMAQGLTGTMDYQIVAVEGYF 213

Qy 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 4

Qy 080704 PRELIMINARY; PRT; 220 AA.
 AC 080704;
 RC 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Xylanase.
 OS Trichoderma sp. SY.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 CX NCBI_TaxID=215577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SY;
 RA Min S.Y., Kim B.G., Ahn J.-H.;
 RA "Purification, Characterization, and cDNA Cloning of Xylanase from

RT Fungus Trichoderma Strain SY.":
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY156910; AAN78423.1; -
 DR GO: GO:0004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR SEQUENCE 220 AA; 23814 MW; 10EB87D5168B05EF CRC64;
 Query Match 85.0%; Score 898; DB 3; Length 220;
 Best Local Similarity 84.2%; Pred. No. 2,4e-61;
 Matches 160; Conservative 11; Mismatches 19; Indels 0; Gaps 0;
 QY 1 QTIQPGTGNNGYFFSYNNDGSGVTTNPGGQFSYVWNSGAFVGGKMGQPGTKKVI 60
 DB 31 QVIGPGFNNNGYYSYNDGSHGVTYTNAGGSFSYVWNSGAFVGGKMGNPSSSTRTI 90
 QY 61 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 120
 DB 91 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 150
 QY 121 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 180
 DB 151 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 210
 QY 181 SSGSASITVS 190
 DB 211 SSGSANINVS 220
 RESULT 5
 Q9UVF9 PRELIMINARY; PRT; 223 AA.
 ID Q9UVF9
 AC Q9UVF9
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
 OS Trichoderma viride.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocremycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5547;
 RN [1]
 RA Fuman-Matarasso N., Cohen E., Avni A.;
 RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
 RT Elicitor Inhibits the b-1,4-Endoxylanase Activity But Not the
 RT Elicitation Activity.", to the EMBL/GenBank/DBJ databases.
 RU Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: AJ012718; CAB60757.1; -
 DR HSSP: P48793; 1XND.
 DR GO: GO:0004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT SIGNAL 1 33
 FT CHAIN 34 223
 FT SEQUENCE 223 AA; 24230 MW; PBF812028FB1212A CRC64;

Query Match 82.3%; Score 869; DB 3; Length 223;
 Best Local Similarity 81.6%; Pred. No. 4.1e-59;
 Matches 155; Conservative 12; Mismatches 23; Indels 0; Gaps 0;
 QY 1 QTIQPGTGNNGYFFSYNNDGSGVTTNPGGQFSYVWNSGAFVGGKMGQPGTKKVI 60
 DB 34 QVIGPGFNNNGYYSYNDGSHGVTYTNAGGSFSYVWNSGAFVGGKMGNPSSSTRTI 93
 QY 61 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 120
 DB 94 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRT 153
 QY 121 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 180
 DB 154 QRVNOPSIIIGTATFYQVSVRRNRSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSANINVS 223
 RESULT 6
 Q12580 PRELIMINARY; PRT; 241 AA.
 ID Q12580
 AC Q12580
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endo-beta1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN CGXB.
 OS Chaetomium gracile.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
 OX NCBI_TaxID=47794;
 RN [1]
 RA MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 RT expression in Aspergillus nidulans.";
 RL Curr. Genet. 29:73-80 (1995).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: D49851; BAA08650.1; -
 DR PIR: S71473; S71473.
 DR HSSP: P36217; 1XVO.
 DR GO: GO:0004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR Glycosidase; Hydrolase; Xylan degradation.
 SO SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;
 Query Match 72.4%; Score 764.5; DB 3; Length 241;
 Best Local Similarity 73.8%; Pred. No. 4.6e-51;
 Matches 135; Conservative 20; Mismatches 27; Indels 1; Gaps 1;
 QY 7 TCVNNGYFFSYNNDGSGVTTNPGGQFSYVWNSGAFVGGKMGQPGTKKVINFSGSY 66
 DB 38 TCVNNGYFFSYNNDGSGVTTNPGGQFSYVWNSGAFVGGKMGQPGTKKVINFSGSY 96
 QY 67 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRTQVNOP 126
 DB 97 NFSGSYNPNNGSYLVGWSKNPLIEYIVENFGTYNPSTGATKLGCVTDCGSVYDIYRTQVNOP 156
 QY 127 SIGTATFYQVSVRRNRSSGSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGSAS 186

Db 157 SIEGISTFYQFWSVQRKSGSVNMAAFNMAAAGLQTHDYQIVATEGYSSGSAT 216
 QY 187 ITV 189
 Db 217 VNV 219

RESULT 7

Q871E8 PRELIMINARY; PRT; 293 AA.
 ID 0871E8
 AC 0871E8
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Probable endo-1, 4-beta-xylanase B.
 GN B8g12.010.
 OS Neurospora crassa.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 CX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX394027; CAD71059.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR Pfam; PF00457; Glyco_hydro_11.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PRODOM; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; FCBP_1.
 DR PROSITE; PS00562; CBD_FUNGAL; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.
 KW Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 293 AA; 30776 MW; D67A81CE65930F26 CRC64;

Query Match 70.3%; Score 742.5; DB 3; Length 293;
 Best Local Similarity 71.0%; Pred. No. 2.8e-49;
 Matches 130; Conservative 25; Mismatches 27; Indels 1; Gaps 1;

QY 7 TGVNNGYFYQWVNDHGVTYTPGQGFVSNMNSGNFVGKGMQPGTKNKVINFSGSY 66
 Db 42 TGTNGYFYFSTWDGQSVRTYBAGQYATWSGNMNGWGGKMGMT-DRTINTYTRY 100
 QY 67 NPNNGSYLSTVYSGRNPLIEYIVENFGTNPSTGATKLGCVTCDSVYDIYTORVNO 126
 Db 101 SPNGNSYLAAYGTRNPLIEYIVENFGTNPSTGATKLGCVTCDSVYDIYTORVNO 160
 QY 127 SICTATFYQWVSRNHRSSGSVNTAHPNMAHQGLTGTMDYQIVAVEGFFSSGSAS 186
 Db 161 SIDGATFYQWVSRQKRTGGSVNMKNHFDWTRSGILGTINYOIVAEIGFFSSGSST 220
 QY 187 ITV 189
 Db 221 INV 223

RESULT 8

Q8J1V6 PRELIMINARY; PRT; 261 AA.
 ID 08J1V6
 AC 08J1V6;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endoxylanase 11A precursor.
 GN XYN1A.
 OS Chaetomium thermophilum.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Chaetomiacae; Chaetomium.
 CX NCBI_TaxID=209285;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mantyla A., Palcheimo M., Hakola S., Leskinen S., Vehmaanpera J.,
 RA Lantto R., Suominen P.;
 RT "Heterologous production of three xylanases from Chaetomium
 thermophilum in Trichoderma reesei";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ508931; CAD48749.1; .
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; ConA_like_1ec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.
 KW Signal; Xylan degradation; Hydrolase; Glycosidase.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 261 ENDOXYLANASE 11A.
 SQ SEQUENCE 261 AA; 27844 MW; 420D625634D7707 CRC64;

Query Match 67.2%; Score 709.5; DB 3; Length 261;
 Best Local Similarity 65.3%; Pred. No. 8.3e-47;
 Matches 124; Conservative 27; Mismatches 38; Indels 1; Gaps 1;
 QY 1 OTI-OPGTVNNGYFYQWVNDHGVTYTPGQGFVSNMNSGNFVGKGMQPGTKNKV 59
 Db 27 OTLTSATGTNGYFYFSTWDGQSVRTYBAGQYATWSGNMNGWGGKMGMTDRTINTYTRY 86
 QY 60 INFSGSYNPNNGSYLSTVYSGRNPLIEYIVENFGTNPSTGATKLGCVTCDSVYDIYR 119
 Db 87 INYTDYPRNNGSYLAAYGTRNPLIEYIVENFGTNPSTGATKLGCVTCDSVYDIYR 146
 QY 120 TORVNOPISTATFYQWVSRNHRSSGSVNTAHPNMAHQGLTGTMDYQIVAVEGFFSSGSAS 179
 Db 147 TORVNOPISTATFYQWVSRNHRSSGSVNTAHPNMAHQGLTGTMDYQIVAVEGFFSSGSAS 206
 QY 180 FSSGSASITV 189
 Db 207 YSSGSATVNV 216

RESULT 9

Q12579 PRELIMINARY; PRT; 219 AA.
 ID 012579
 AC 012579;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-beta1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN CGXA.
 OS Chaetomium gracile.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Chaetomiacae; Chaetomium.
 CX NCBI_TaxID=47794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 expression in Aspergillus nidulans";
 RL Curr. Genet. 29:73-80(1995).
 CC -I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -I- PATHWAY: XILAN DEGRADATION.

[illegible]

Query Match	Similarity	66.7%	Pred. No. 2,1e-45	Matches	122	Conservative	26	Mismatches	34	Indels	1	Gaps	1
Qy	7	TCYNNNGYFYSYVNDGHHGVYTTNPGGQF	SVNMSNSGNFVGKGMQPTKXKVINFSGSY	66									
Db	50	TCYNNNGYFYSYVNDGHHGVYTTNPGGQF	SVNMSNSGNFVGKGMQPTKXKVINFSGSY	108									
Qy	67	NPNGNSYFYSYVGMGRNPLIEYIYVENFSTYV	PSGATATLGEVTCGSGSYVDIYRTORVNP	126									
Db	109	NPNGNSYFYSYVGMGRNPLIEYIYVENFSTYV	PSGATATLGEVTCGSGSYVDIYRTORVNP	168									
Qy	127	SIIGTATPQYQWYSVRNRHSSGSYNTACHFN	AMAQHGTLTGMDYQIYVAVEGYFSSGSAS	186									
Db	169	SIIGTATPQYQWYSVRNRHSSGSYNTACHFN	AMAQHGTLTGMDYQIYVAVEGYFSSGSAS	228									
Qy	187	ITV	189										
Db	229	ITV	231										
RESULT 11													
Q9C1R2	ID	PRELIMINARY	PRT	295	AA								
AC	Q9C1R2												
DT	01-JUN-2001	(TREMBLrel. 17, Created)											
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)											
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)											
DE	Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).												
GN	Xy5.												
OS	Fusarium oxysporum f. sp. lycopersici.												
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;												
CC	Hypocotomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.												
OX	NCBI_taxid=59765;												
RP	SEQUENCE FROM N.A.												
RA	Hera C., Gomez-Gomez E., Roncero M.;												
RT	"Cloning and characterization of two family 11 xylanase genes in												
RL	Fusarium oxysporum f. sp. lycopersici."												
CC	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.												
CC	-1 CATALYTIC ACTIVITY: ENDOPOLYMERASE OF 1,4-BETA-D-XYLOSIDIC												
CC	LINKAGES IN XYLANS.												
CC	-1 PATHWAY: XYLAN DEGRADATION.												
CC	-1 SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL												
CC	HYDROLASES).												
DR	EMBL; AF246830; AAK27974.1; -.												
DR	HSBP; O43697; IYNA.												
DR	GO; GO:0004553; P:hydrolyase activity, hydrolyzing O-glucosyl . . .; IEA.												
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.												
DR	InterPro; IPR008985; Cona. like lec gl.												
DR	InterPro; IPR001137; Glyco. hydro. 11.												
DR	Pfam; PF00457; Glyco. hydro. 11; 1.												
DR	PRINTS; PR00911; GLHYDRLASE1.												
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.												

Db 159 SLDGLTQTFQOQYWSVRQKHSTGSSVDTGLHFDAMEAGKGLGTHDYQILLATGEGYSSSSH 218
QY 187 ITVS 190
: |||
Db 219 MTVS 222

RESULT 12
Q9HEZ0
ID Q9HEZ0 PRELIMINARY;
PRT; 290 AA.

DT 01-MAR-2001 (TReMBLrel_16, Created)
DT 01-MAR-2001 (TReMBLrel_16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel_25, Last annotation update)
DE Endo-1,4- β -Xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYNB.
OS Phanerochaete chrysosporium.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Asphyliophorales; Corticiaceae; Phanerochaete.
OX NCBI_TaxID=5306;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=ME446;
RA Kuan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
RT "Molecular characterization and expression analysis of two endo-1,4- β -
RT xylanase genes from Phanerochaete chrysosporium";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL, AF301904; AAG4994.1; -.
DR HSPD, P00725; IAZ6.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing α -glycosyl . . .; IEA
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR000254; CBD_fungal.
DR InterPro: IPR008985; ConA_like_lac_g1.
DR InterPro: IPR001137; glyco_hydro_11.
DR Pfam: PF00734; CBM_1_1.
DR Pfam: PF00457; Glyco_hydro_11_1.
DR PRINTS: PR00911; GLHYDLASE11.
DR ProDom: PD001821; CBD_fungal_1.
DR SMART: SM00236; FCBD; 1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Glycosidase; Hydrolase; Xylan degradation.
QJ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match	64.5%	Score 681.5;	DB 3;	Length 290;
Best Local Similarity	63.7%	Pred. No. 1.3e-4;		
Matches 121; Conservative	26;	Mismatches 42;	IndeIs 1;	Gaps 1;

[illegible]

RESULT 13
Q9HEY9

ID	Q9HEV9	PRELIMINARY;	PRT;	290 AA.
AC	Q9HEV9;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Endo-1,4-B-xylinanase B (EC 3.2.1.8) (Endo-1,4-beta-xylinanase).			
EN	XFN3.			

Query Match	64.5%;	Score 681.5;	DB 3;	Length 290;
Best Local Similarity	63.7%;	Pred. No. 1.3e-44;		
Matches 121;	Conservative 26;	Mismatches 42;	Indels 1;	Gaps 1;

QY	1	QTLQPTGVNNQYFPYSVYNDGHGAVLYTNGGQGPQSVYMWSSGKGFVGGKMGQPTKRV	60
Db	34	QSLPACTGTTNNQYFYSFMTDGGGSLTYNNGRAGEISVTWMSADNFVAGKGNPESA-QAI	92
QY	61	NFSGSYNPGNSYLSVYGMNRPLLEYIVENFGTNPSTGATKLGVEYTDGDSYYDIYRT	120
Db	93	SFLPANYQPRGNSYLSVYGMSTNPLVEYIYLEDPTGYNPAVSLTKGTLTSDGATYDYEG	152
QY	121	QRNQSSTIGLTFIQYMSVRPNHHSSGSVNTACHFNMAOHGLTGLTMDQIYAVBGYF	180
Db	153	TRNNEPSIGLTFIQYMSIRSRSKSSGSSITVTANFPAWKGLGLEGTENQIYATGQYQ	212
QY	181	SGGSASITVS-190	
Db	213	SGGSSTIVN-222	

RESULT 14	
000263	
ID 000263	PRELIMINARY; PRT; 227 AA.
AC 000263;	
DT 01-NOV-1996	(TREMBLrel. 01, Created)
DT 01-NOV-1996	(TREMBLrel. 01, last sequence update)
DT 01-OCT-2003	(TREMBLrel. 25, last annotation update)
DE xylanase1, 4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).	
DE Ascochyta pisi.	
CC Eukaryota; Fungi; Ascomycota; Pezizomycotina;	
CC mitosporic Pezizomycotina; Ascochyta.	

OX NCBI_TaxID=47971;
 RN
 RE SEQUENCE FROM N.A.
 RA Lubbeck P.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.;
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the
 RT phytopathogenic fungus *Ascochyta blight* lib.,"
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASE OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: Z68891; CA93120.1; -.
 DR HSP: 043097; 1YNA.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like_g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR KEGG: Glycosidase; Hydrolyase; Signal; Xylan degradation.
 KW SIGNAL
 FT SIGNAL 1
 SQ SEQUENCE 227 AA; 24010 MW; 692A51FAE035CF0F CRC64;
 Query Match 64.1%; Score 676.5; DB 3; Length 227;
 Best Local Similarity 65.3%; Pred. No. 2.4e-44;
 Matches 126; Conservative 20; Mismatches 42; Indels 5; Gaps 2;
 QY 2 TIQPGT---GYNNGYYSYVNDGHHGVTYNGPGGFSVWNSNGFVGKGMQPGTKN 57
 DB 34 TARAGTPSSQCTHNGCFYSWMTDGAQATYNGAGGSYSVNMKTGKLVGKGMPPGA- 92
 QY 58 KVINFGSYNDGNSYSYVNGMSNPLEIYVENFGTYNPSTGATKGEVTCDDGVYDI 117
 DB 93 RTIYSGYSYSSGNSYLAIVGWTNPLEIYVENFGTYNPSTGATKGEVTCDDGVYDI 152
 QY 118 YRTQVNPSTIGTATFYQVWSVRRNHRSSGSVNTACHFNMAOHGLTGTMDYQIYAVE 177
 DB 153 AQTQRTNPSTIGTATFYQVWSVRRNHRSSGSVNTACHFNMAOHGLTGTMDYQIYAVE 212
 QY 178 GYFSSGSASITVS 190
 DB 213 GYFSSGSASITVN 225
 RESULT 15
 Q9UVZ3
 ID Q9UVZ3 PRELIMINARY; FRT; 227 AA.
 AC Q9UVZ3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYL1.
 OS Secosphaeria turcica.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Setosphaeria.
 OX NCBI_TaxID=93612;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H2.
 RA Degefu Y., Paulin L., Perenen U., Lubbeck P.S.;
 RT "Cloning, sequencing and expression of a xylanase gene from the maize
 RT pathogen *Helminthosporium turcicum* Pass.,"
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASE OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: AJ238895; CAB52417.1; -.

DR HSP: 043097; 1YNA.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_like_g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR KEGG: Glycosidase; Hydrolyase; Signal; Xylan degradation.
 KW SIGNAL
 FT SIGNAL 1
 SQ SEQUENCE 227 AA; 24123 MW; BA86FC075EE5306E CRC64;
 Query Match 63.5%; Score 670.5; DB 3; Length 227;
 Best Local Similarity 64.2%; Pred. No. 7e-44;
 Matches 122; Conservative 22; Mismatches 45; Indels 1; Gaps 1;
 QY 1 QTIQPGTGYNNGYYSYVNDGHHGVTYNGPGGFSVWNSNGFVGKGMQPGTKNXYI 60
 DB 37 QSTPNQEGHNGCFYSWSDGAGATYNGAGGSYSVNMKTGKLVGKGMPPGA-RTI 95
 QY 61 NFGSYNDGNSYSYVNGMSNPLEIYVENFGTYNPSTGATKGEVTCDDGVYDIYRT 120
 DB 96 TYSQYNPNGNSYLAIVGWTNPLEIYVENFGTYNPSTGATKGEVTCDDGVYDIYRT 155
 QY 121 QVNPSTIGTATFYQVWSVRRNHRSSGSVNTACHFNMAOHGLTGTMDYQIYAVEGYF 180
 DB 156 TRTNQPSLIGTATFYQVWSVRRNHRSSGSVNTACHFNMAOHGLTGTMDYQIYAVEGYF 215
 QY 181 SSGSASITVS 190
 DB 216 SSGSASITVN 225
 Search completed: June 30, 2004, 19:43:40
 Job time : 33 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:25:28 ; Search time 53 Seconds

(without alignments)
1012.906 Million cell updates/sec

Title: US-09-856-025B-63

Perfect score: 1058

Sequence: 1 QTIQGTGTNNGYFYFSYND.....YQIVAVEGYFSSGSASITVS 190

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_250a04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003s.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1031	97.4	190	2	AAW60743 Xylanase
2	1031	97.4	190	3	AAy99680 T. reesei
3	1031	97.4	190	5	AAE18452 Trichoder
4	1031	97.4	190	7	AAO30259 Trichoder
5	1031	97.4	223	2	AAr47122 PI 9.0 en
6	1031	97.4	223	2	AAW67567 T. reesei
7	1029	97.3	190	3	AAy99735 Mutant T.
8	1028	97.2	190	5	AAE18470 Trichoder
9	1028	97.2	190	5	AAE18495 Trichoder
10	1028	97.2	190	7	AAO30300 Trichoder
11	1027	97.1	190	7	AAO30303 Trichoder
12	1027	97.1	190	7	AAO30301 Trichoder
13	1026	97.0	190	3	AAE18451 Trichoder
14	1026	97.0	190	5	AAE18467 T. reesei
15	1026	97.0	190	7	AAO30304 Trichoder
16	1025	96.9	190	7	AAO30289 Trichoder
17	1024	96.8	190	7	AAW60284 Modified
18	1024	96.8	190	5	AAE18471 Trichoder
19	1024	96.8	190	7	AAO30279 Trichoder
20	1023	96.7	190	5	AAE18496 Trichoder
21	1023	96.7	190	7	AAO30302 Trichoder
22	1022	96.6	190	7	AAO30280 Trichoder
23	1021	96.5	190	2	AAW60744 Xylanase
24	1021	96.5	190	3	AAy99681 T. viride
25	1021	96.5	190	5	AAE18453 Trichoder

26	1020	96.4	190	7	AAO30306 Trichoder
27	1018	96.2	190	7	AAO30307 Trichoder
28	1015	95.9	190	7	AAO30305 Trichoder
29	1015	95.9	223	2	AAW57422 Amino aci
30	1011	95.6	190	7	AAO30293 Trichoder
31	1009	95.4	190	5	AAE18472 Trichoder
32	1009	95.4	190	7	AAO30287 Trichoder
33	1009	95.4	190	7	AAO30294 Trichoder
34	1008	95.3	190	3	AAE18473 Trichoder
35	1008	95.3	190	5	AAO18644 T viride
36	1007	95.2	190	7	AAO30297 Trichoder
37	1006	95.1	190	5	AAE18476 Trichoder
38	1005	95.0	190	7	AAO30298 Trichoder
39	1004	94.9	190	7	AAO30292 Trichoder
40	1003	94.8	190	5	AAE18475 Trichoder
41	1003	94.8	190	5	AAE18474 Trichoder
42	1003	94.8	190	5	AAE18482 Trichoder
43	1003	94.8	190	7	AAO30288 Trichoder
44	1002	94.7	190	5	AAE18473 Trichoder
45	1000	94.5	190	5	AAE18478 Trichoder

ALIGNMENTS

RESULT 1
AAW60743
ID AAW60743 standard; protein; 190 AA.
XX
AC AAW60743;
XX
AC 17-OCT-2003 (revised)
DT 02-SEP-1998 (first entry)
XX
DE Xylanase II of Trichoderma reesei.
XX
KM Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KM thermotolerance; bleach; wood pulp; processing; wheat; maize;
KM digestibility-improving animal feed additive; starch production; mutant.
OS Hypocrea jeorina.
XX
EM EP828002-A2.
XX
PD 11-MAR-1998.
XX
PF 05-SEP-1997; 97EP-00115412.
PR 09-SEP-1996; 96US-00709912.
PA (CANNA) NAT RES COUNCIL CANADA.
PI Sung WL, Yaguchi M, Ishikawa K;
DR WPI; 1998-161100/15.
XX
PS Modified xylanase enzymes - useful for improving wood pulp bleaching,
PT etc.
XX Disclosure; Page 48; 84pp; English.
CC AAW60728-44 represent family 11 xylanases. The specification describes a
CC method for modifying a Family 11 xylanase to improve its thermophilicity,
CC alkalophilicity and/or thermotolerance. This method comprises
CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase
CC II or corresponding aligned amino acids of another Family 11 xylanase,
CC replacement of one or more amino acid sequences in the N-terminal region
CC with corresponding aligned sequences from another Family 11 xylanase to
CC form a chimeric xylanase and/or upstream extension of the N terminus by
CC addition of upto 10 amino acids. The modified xylanases are useful for
CC improving the bleachability of wood pulp by treatment at 55-75 degrees
CC Celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as
CC digestibility-improving animal feed additives. They might also be useful

CC in the processing of wheat or maize for starch production. (updated on 17
 CC -Oct-2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 2; Length 190;
 Best Local Similarity 98.4%; Pred. No. 6,9e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTIQPGTGNNGCFYFYVNDHGCVTYTNGPGQPSVNMNSGNFVGKGMQPGTKNKVI 60
 DB 1 OTIQPGTGNNGCFYFYVNDHGCVTYTNGPGQPSVNMNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFGSGYNPNKNSYLSVYCGMSRNPLEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120
 DB 61 NFGSGYNPNKNSYLSVYCGMSRNPLEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120
 QY 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAOGLTLGTMDYQIYAVEGYF 180
 DB 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAOGLTLGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 2
 AAY9680
 ID AAY9680 standard; protein; 190 AA.
 XX
 AC AAY9680;
 DT 12-SEP-2003 (revised)
 DT 28-SEP-2000 (first entry)
 XX
 DE T. reesei xylanase, Xyn II.
 XX
 KM Xylanase; animal feed; digestion efficiency; thermostable;
 KM feed pelleting; enzyme; Xyn A; Xyn B; Xyn C; Xyn I; Xyn II.
 XX
 OS Hypocrea jecorina.
 XX
 PN WO200029587-A1.
 XX
 PD 25-MAY-2000.
 XX
 PF 16-NOV-1999; 99MO-CA001093.
 XX
 PR 16-NOV-1999; 98US-0108504P.
 XX
 PA (IOGE-) IOGEN CORP.
 XX
 PI Sung WL, Tolan JS;
 XX
 DR WPI; 2000-387799/33.
 DR N-PSDB; AAA48219.
 XX
 PT Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.
 XX
 PS Disclosure; Fig 1; 86pp; English.
 XX
 CC Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*
 CC reesei, is a xylanase Family 11 member. The xylanases of Family 11 have
 CC several properties suitable for feed applications, however, they lack the
 CC thermostability required to survive food pelleting. The present sequence
 CC was used to identify non-conserved residues in Family 11 xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.
 CC As a result various thermostable xylanases were identified (AAY9683,
 CC AAY9684, AAY9685, AAY9686, AAY9735 and AAY9736) which would be
 CC useful for animal feeds, especially poultry and swine feed. (updated on
 CC 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 3; Length 190;
 Best Local Similarity 98.4%; Pred. No. 6,9e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 OTIQPGTGNNGCFYFYVNDHGCVTYTNGPGQPSVNMNSGNFVGKGMQPGTKNKVI 60
 DB 1 OTIQPGTGNNGCFYFYVNDHGCVTYTNGPGQPSVNMNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFGSGYNPNKNSYLSVYCGMSRNPLEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120
 DB 61 NFGSGYNPNKNSYLSVYCGMSRNPLEYIIVENFGTNPSTGATKLGECTSDGSVDIYRT 120
 QY 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAOGLTLGTMDYQIYAVEGYF 180
 DB 121 QRYNOPSIIIGTATFYQVMSVRNRHSSGSVNTANHFNCMAOGLTLGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 3
 AAE18452
 ID AAE18452 standard; protein; 190 AA.
 XX
 AC AAE18452;
 DT 29-AUG-2003 (revised)
 DT 16-MAY-2002 (first entry)
 XX
 DE *Trichoderma reesei* xylanase (T-X), Xyn II.
 XX
 KM Modified xylanase; thermostability; alkalophilicity; industrial process;
 KM pulp manufacture; poultry; swine feed; enzyme; Xyn II.
 XX
 OS Hypocrea jecorina.
 XX
 PN WO200192487-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 31-MAY-2001; 2001MO-CA000769.
 XX
 PR 31-MAY-2000; 2000US-0213803P.
 XX
 PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 XX
 DR WPI; 2002-171435/22.
 DR N-PSDB; AAD29410.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 XX
 PS Disclosure; Page 80-81; 109pp; English.
 XX
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 5; Length 190;
 Best Local Similarity 98.4%; Pred. No. 6.9e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGFYFSYMNDSGHGVTYTNPGGQFSYWNNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTYNNNGFYFSYMNDSGHGVTYTNPGGQFSYWNNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSYVGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSYVGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHRSRGSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHRSRGSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 4
 AA030259
 ID AA030259 standard; protein; 190 AA.

XX AA030259;

DT 23-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)

DE Trichoderma reesei xylanase II enzyme (Trx).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KM pulp manufacture; poultry feed; swine feed; enzyme.

OS Hypocrea jecorina.

XX WO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002WO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL.

XX WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
 PT thermophilicity, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.

PS Claim 1; Fig 2; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved
 CC thermophilicity, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 97.4%; Score 1031; DB 7; Length 190;
 Best Local Similarity 98.4%; Pred. No. 6.9e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNNGFYFSYMNDSGHGVTYTNPGGQFSYWNNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTYNNNGFYFSYMNDSGHGVTYTNPGGQFSYWNNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSYVGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSYVGMSRNPLEIYIYVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYWSVRNRHRSRGSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYWSVRNRHRSRGSVNTANHFNCMAQCHGLTGTMDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 5
 AAR47122
 ID AAR47122 standard; protein; 223 AA.

XX AAR47122;

DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-JUN-1994 (first entry)

DE pl 9.0 endoxylanase.

XX Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pl 5.5;

KM pl 9.0; xln1; xln2; endoxylanase.

XX Hypocrea jecorina; QM6A.

OS Key Location/Qualifiers

XX Cleavage-site 19..20

XX Protein 34..223

XX Modified-site 71

XX Peptide /label= N-glycosylation_site

XX Modified-site 83..89

XX Active-site /note= "sequence used for prepn. of PCR primer"

XX Active-site 119

XX Active-site /note= "Glu proposed to be involved with an active site"

XX Active-site 210

XX Active-site /note= "Glu proposed to be involved with an active site"

XX W09324621-A1.

XX 09-DEC-1993.

XX 24-MAY-1993; 93WO-FI000221.

XX 29-MAY-1992; 92US-00689893.

XX (ALKO-) ALKO OY AB.

XX Suominen P, Nevalainen H, Saarelainen R, Palohelmo M, Lahtinen T,
 PI Fagerstrom R,
 XX WPI; 1993-405812/50.
 DR N-PSDB; AA054775.
 XX

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed
 PI industry - comprising sequence encoding aminoacid sequence of T. reesei
 PI 5.5 xylanase.

PS Claim 3; Page 77-78; 11pp; English.

CC The T. reesei xln2 gene coding for the pI 9.0 endoxylanase was isolated
 CC from the wild-type strain QM6a. The gene contains one intron of 108
 CC nucleotides and codes for a protein of 223 amino acids in which two
 CC putative N-glycosylation target sites were found. Three different T.
 CC reesei strains were transformed by targeting a construct composed of the
 CC xln2 gene with its own promoter to the endogenous chb1 locus. Highest
 CC overall prodn. levels for xylanase were obtained using the T. reesei
 CC ALKO2721, a genetically engineered strain, as a host. Integration into
 CC the chb1 locus was not required for enhanced expression under xln2
 CC promoter. (Updated on 25-MAR-2003 to correct PI field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)

CC Sequence 223 AA;

Query Match 97.4%; Score 1031; DB 2; Length 223;
 Best Local Similarity 98.4%; Pred. No. 8.4e-87;
 Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVMSNSGNFVGKGMOPGTKNKVI 60
 DB 34 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVMSNSGNFVGKGMOPGTKNKVI 93
 QY 61 NFGSGYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
 DB 94 NFGSGYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 153
 QY 121 QRVNOPSIIIGTATFYQVWSVRNRHSSGGSVNTAHNFNCMAQCHGLTLGTMQYQIVAVEGYF 180
 DB 154 QRVNOPSIIIGTATFYQVWSVRNRHSSGGSVNTAHNFNCMAQCHGLTLGTMQYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 6

AAW67567
 ID AAW67567 standard; protein; 223 AA.

AC AAW67567;

DT 17-OCT-2003 (revised)

DT 02-MAR-1999 (first entry)

DE T. reesei xylanase II protein.

KW Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;

KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.

OS Hypocrea jecorina.

FT Key Location/Qualifiers

FT Peptide 1..19 /note= "primary signal peptide"

FT Peptide 20..33 /note= "propeptide"

FT Protein 33..223 /note= "mature xylanase II protein"

FT Modified-site 71 /note= "N-glycosylated"

FT Modified-site 94 /note= "N-glycosylated"

FT Active-site 119 /note= "active site residue"

FT Active-site 210 /note= "active site residue"

XX US8937515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1992; 92US-00889893.

XX 24-MAY-1993; 93WO-FI000221.

XX 18-JUN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTIOET OY.

XX Paloheimo M, Nevalainen H, Saarelainen R, Fagerstrom R;

XX N-PDSB; AAW81332.

XX WPI; 1999-023453/02.

XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for

XX recombinant production of the enzyme, for use in paper and pulp

XX production.

XX Claim 3; Fig 3A-B; 52pp; English.

XX This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)

XX which has an isoelectric point (pI) of 9. The coding sequence was

XX isolated by reverse transcription PCR using the primers AAW81333-V81335

XX based on amino acid sequence derived from the N-terminal of the purified

XX protein. The encoded protein contains a 33 amino acid propeptide sequence

XX with a primary signal peptide cleavage site between residues 19-20. The

XX mature protein comprises 190 amino acids with a calculated molecular

XX weight of 20.8 kD. The enzymes are used in the degradation of the polymer

XX xylan, one of the most abundant carbohydrate components in plants. This

XX is especially useful in the paper and pulp making industry. (Updated on

XX 17-OCT-2003 to standardise OS field)

XX Sequence 223 AA;

XX Query Match 97.4%; Score 1031; DB 2; Length 223;

XX Best Local Similarity 98.4%; Pred. No. 8.4e-87;

XX Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVMSNSGNFVGKGMOPGTKNKVI 60

DB 34 QTIQPGTGYNNGYFYSYWMDHGVTYTNPGGQFSYVMSNSGNFVGKGMOPGTKNKVI 93

QY 61 NFGSGYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120

DB 94 NFGSGYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 153

QY 121 QRVNOPSIIIGTATFYQVWSVRNRHSSGGSVNTAHNFNCMAQCHGLTLGTMQYQIVAVEGYF 180

DB 154 QRVNOPSIIIGTATFYQVWSVRNRHSSGGSVNTAHNFNCMAQCHGLTLGTMQYQIVAVEGYF 213

QY 181 SSGSASITVS 190

DB 214 SSGSASITVS 223

RESULT 7

AAW9735
 ID AAW9735 standard; protein; 190 AA.

AC AAW9735;

DT 12-SEP-2003 (revised)

DT 28-SEP-2000 (first entry)

DE Mutant T. reesei xylanase, Trx-162H.

KW Xylanase; animal feed; digestion efficiency; thermostable;

KW		feed pelleting; enzyme; mutant; mutein; Xyn A; Xyn B; Xyn; Xyn C; Xyn I;
XV	Xyn II.	
XX	Hypocrea jecorina.	
OS	WO200029587-A1.	
PN	25-MAY-2000.	
PD		
XX	16-NOV-1999; 99MO-CA001093.	
PF		
XX	16-NOV-1998; 98US-0108504P.	
PR		
PA	(IOGE-) IOGEN CORP.	
XX	Sung WL, Tolan JS;	
PI	WPI: 2000-387799/33.	
DR		
XX	Thermostable xylanases useful for preparing animal feeds especially	
PT	poultry or swine feed, exhibits optimal activity under physiological	
PT	conditions.	
PS	Example 3; Page; 86pp; English.	
XX		
CC	Xylanase enzymes are added to animal feeds to increase the efficiency of	
CC	digestion and assimilation of nutrients. Xylanases are preferentially	
CC	added during the feed pelleting process. To survive the pelleting process	
CC	and to have optimum activity in the animal, the xylanase needs to have	
CC	high thermostability, with optimum activity at physiological pH and	
CC	temperature. Xylanase Xyn II, from Trichoderma reesei, is a xylanase	
CC	Family II member. The xylanases of Family II have several properties	
CC	suitable for feed applications, however, they lack the thermostability	
CC	required to survive food pelleting. The present sequence was used to	
CC	identify non-conserved residues in Family II xylanases which could be	
CC	mutated to introduce desirable properties e.g. thermostability. As a	
CC	result various thermostable xylanases were identified (the present	
CC	sequence, AA199736, AA199737, AA199738, AA199739 and AA199740) which	
CC	would be useful for animal feeds, especially poultry and swine feed.	
CC	Note: the present sequence is not shown in the specification but is	
CC	derived from the T. reesei wild-type xylanase sequence given in figure 1	
CC	(see AA199680). (Updated on 12-SEP-2003 to standardise OS field)	
XX		
SO	Sequence 190 AA;	
	Query Match 97.3%; Score 1029; DB 3; Length 190;	
	Best Local Similarity 97.9%; Pred. No. 1.le-86;	
	Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;	
OY	1 OTIQPGTGVNNGCYFEFSYNNDDHGCGTYTNNGPPGGQGSVNWSNSGNFVGKMGMPGTRNKVI 60	
DB		
	1 OTIQGTGFNNNGYFFSYNDGDHGVYTYNNGPGQGSVNWSNSGNFVGKGMPGTRNKVI 60	
OY	61 NFSGSYNENGSYSLVYSGMSRNPLEYIIVENFGTYNESTGATKKJGECTSDSVDIYRT 120	
DB	61 NFSGSYNENGSYSLVYSGMSRNPLEYIIVENFGTYNESTGATKKJGCVTSIDSVDIYRT 120	
OY	121 QRANOPSLITGATLFCQYWSVVRNRHSSSGSVNTAHFNPCMAOGLTLGTMDIYTVAVEGYF 180	
DB	121 QRANOPSLITGATLFCQYWSVVRTRRSSSGSVNTAHFNPMACHGLTLGTMDYOIVAEGYF 180	
OY	181 SSGSASITVS 190	
DB	181 SSGSASITVS 190	
	RESULT 8	
	AAE18470	
ID	AAE18470 standard; protein; 190 AA.	
AC	AAE18470;	
XX		
JT	16-MAY-2002 (first entry)	

DE		Trichoderma reesei xylanase mutant, Trx-75A.	. . .
XX			
KW		Modified xylanase; thermostability; alkalophilicity; industrial process;	
RN		pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.	
XX			
OS		Hypocrea jecorina.	
CS		Synthetic.	
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference	/note= "wild type Ser substituted with Ala"	
PT			
PX			
PN		WO200192487-A2.	
XX			
XX		06-DEC-2001.	
XK			
PF		31-MAY-2001; 2001WO-CAN000769.	
XX			
PR		31-MAY-2000; 2000US-0213803P.	
XX			
PA	(CANA) NAT RES COUNCIL CANADA.		
PL			
FI	Sung WL;		
DR		WP1; 2002-171435/22.	
XX			
PT	Modified xylanase exhibiting increased thermostability and		
XX	alkalophilicity useful for industrial processing e.g. for pulp		
PT	manufacturing.		
PS			
Claim 42; Page; 109pp; English.			
CC	The present invention relates to a modified xylanase exhibiting increased		
XX	thermostability and alkalophilicity. Modified xylanase is useful in		
CC	industrial process such as pulp manufacturing. Modified xylanase is also		
CC	useful for bleaching of pulp, processing of precision devices and		
CC	improved digestibility of poultry and swine feed. Modified xylanase has		
CC	exhibits improved thermophlicity and/or alkalophilicity in comparison to		
CC	xylanase (TRX) mutant. Note: The present sequence is shown in the		
CC	specification but is derived from wild type xylanase referred as SEQ ID		
CC	No. 16 (AAE18452) and shown in page 80-81 of the specification		
XX			
CX	Sequence 190 AA:		
SEQ			
Query Match	97.2%; Score 1028; DB 5; Length 190;		
Best Local Similarity	97.9%; Pred. No. 1,3e-86;		
Matches 186; Conservative	1; Mismatches 3; Indels - 0; Gaps 0		
QY	1 OTTQPCTGNNNGFYFSYNNDGGVTTYTNPGFGGFSVNWNSGNFVGKGGMOPGTNRKYI	60	
DB	1 OTTPGTGYNNNYFFSYWNDDHGVTYTNGDGPJGSFNWSNNGNFVGKKMCPGTNRKYI	60	
QY	61 NREGSVPNPKSNYSIVSGMSRNPLEIEVIYVENRSTNPSCARKLRBCSDSVVDIYRT	120	
DB	61 NREGSATNPKNISYLAVYCMSRPLELYIYENPETNIIPSGATRLGVTSDSGDVIDIYRT	120	
QY	121 QRVNOPSIIIGTAIFYQYVSVRNRHSRGSSVTANHFNCAOHGLITGMTDYCIVAVEGYF	180	
DB	121 QRVNQSIIIGTAGTFYQYVSVMRRHRSSGVNTAHFNAMAOQGILGITMDYQIVAIVEGYF	180	
QY	181 SSGSASTITVS 190		
DB	181 SSGSASTITVS 190		

Accession	Protein Name	Organism	Length (aa)	Score	DB	Length (aa)	Score	DB
U00001	16-MAY-2002 (first entry)	XX	165H	97.2%	1028	190	97.9%	1028
U00002	Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.	XX	165H	97.9%	1028	190	97.9%	1028
U00003	Modified xylanase; thermostability; alkalophilicity; industrial process; pulp manufacture; poultry; swine feed; enzyme; mutant; mutenim.	XX	165H	97.9%	1028	190	97.9%	1028
U00004	Hypocrea jecorina.	XX	165H	97.9%	1028	190	97.9%	1028
U00005	Synthetic.	XX	165H	97.9%	1028	190	97.9%	1028
U00006	Key	XX	165H	97.9%	1028	190	97.9%	1028
U00007	Location/Qualifiers	XX	165H	97.9%	1028	190	97.9%	1028
U00008	Misc-difference 161	XX	165H	97.9%	1028	190	97.9%	1028
U00009	/note= "Wild type Gln substituted with Arg"	XX	165H	97.9%	1028	190	97.9%	1028
U00010	Misc-difference 162	XX	165H	97.9%	1028	190	97.9%	1028
U00011	/note= "Wild type Gln substituted with His"	XX	165H	97.9%	1028	190	97.9%	1028
U00012	Misc-difference 165	XX	165H	97.9%	1028	190	97.9%	1028
U00013	/note= "Wild type Thr substituted with His"	XX	165H	97.9%	1028	190	97.9%	1028
U00014	NO200192487-A2.	XX	165H	97.9%	1028	190	97.9%	1028
U00015	06-DEC-2001.	XX	165H	97.9%	1028	190	97.9%	1028
U00016	31-MAY-2001; 2001WO-CAD00769.	XX	165H	97.9%	1028	190	97.9%	1028
U00017	31-MAY-2000; 2000US-0213803P.	XX	165H	97.9%	1028	190	97.9%	1028
U00018	(CANA) NAT RES COUNCIL CANADA.	XX	165H	97.9%	1028	190	97.9%	1028
U00019	Sung WL;	XX	165H	97.9%	1028	190	97.9%	1028
U00020	WPI; 2002-171435/22.	XX	165H	97.9%	1028	190	97.9%	1028
U00021	Modified xylanase exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing.	XX	165H	97.9%	1028	190	97.9%	1028
U00022	Claim 42; Page; 103pp; English.	XX	165H	97.9%	1028	190	97.9%	1028
U00023	The present invention relates to a modified xylanase exhibiting increased thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase has exhibits improved thermostability and/or alkalophilicity in comparison to corresponding native xylanase. The present sequence is not shown in the specification but is derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification	XX	165H	97.9%	1028	190	97.9%	1028
U00024	Sequence 190 AA;	XX	165H	97.9%	1028	190	97.9%	1028
U00025	Query Match	XX	165H	97.9%	1028	190	97.9%	1028
U00026	Best Local Similarity	XX	165H	97.9%	1028	190	97.9%	1028
U00027	Matches 166; Conservative 1; Mismatches 3; Indels 0; Gaps 0	XX	165H	97.9%	1028	190	97.9%	1028
U00028	1 QTTQPGTGYNNGFFISYANDGHGVTYNNNGGQGFQVYWSNSGNFVGGKMGQGTGKXKI 60	XX	165H	97.9%	1028	190	97.9%	1028
U00029	1 QTTQPGTGYNNGFFISYANDGHGVTYNNNGGQGFQVYWSNSGNFVGGKMGQGTGKXKI 60	XX	165H	97.9%	1028	190	97.9%	1028
U00030	61 NFGSGVNPQNSNLSLYSGNSRNP.L.EYIIVENFGYNPSTGATLGGCTSDGSVDYIYRT 120	XX	165H	97.9%	1028	190	97.9%	1028
U00031	61 NFGSGVNPQNSNLSLYSGNSRNP.L.EYIIVENFGYNPSTGATLGGCTSDGSVDYIYRT 120	XX	165H	97.9%	1028	190	97.9%	1028
U00032	61 NFGSGVNPQNSNLSLYSGNSRNP.L.EYIIVENFGYNPSTGATLGGCTSDGSVDYIYRT 120	XX	165H	97.9%	1028	190	97.9%	1028
U00033	121 QRVNQPISIICTATFYQYVSVRRNHS SSGSVTANHFNCMAOGLTLGTMDYQIVAVEGTF 180	XX	165H	97.9%	1028	190	97.9%	1028
U00034	121 QRVNQPISIICTATFYQYVSVRRNHS SSGSVTANHFNCMAOGLTLGTMDYQIVAVEGTF 180	XX	165H	97.9%	1028	190	97.9%	1028
U00035	121 QRVNQPISIICTATFYQYVSVRRNHS SSGSVTANHFNCMAOGLTLGTMDYQIVAVEGTF 180	XX	165H	97.9%	1028	190	97.9%	1028
U00036	181 SSGSASTIVS 190	XX						

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RESULT 10
AAO30300
ID AAO30300 standard; protein; 190 AA.
XX
AC AAO30300;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (S7SA).
XX
KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
   pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutetrn.
XX
OS Hypocrea jecorina.
XX
SX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 75 /note= "Wild type Ser substituted with Ala"
FT FT
XX
EN WC2003046169-A2.
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2002; 2002WC-CA001758.
XX
PR 21-NOV-2001; 2001US-00930874.
XX
EA (CANA ) NAT RES COUNCIL CANADA.
XX
PI Sung WL;
DR WPI; 2003-513647/48.
XX
PT Novel modified xylanase useful in industrial process, exhibits improved
   thermophilicity, alkalophilicity and expression efficiency, in comparison
   to a corresponding native xylanase from Trichoderma reesei.
XX
PS Example 1; Page; 105pp; English.
XX
CC The invention relates to modified xylanase enzyme which exhibits improved
   thermophilicity, alkalophilicity and expression efficiency, in comparison
   to a corresponding native Trichoderma reesei xylanase (Trx). The modified
   xylanase is useful in an industrial process e.g. pulp manufacturing. It
   is useful for the bleaching of pulp, processing of precision devices and
   for improving digestibility of poultry and swine feed. The present
   sequence is Trichoderma reesei xylanase II mutant protein. Note: This
   sequence is not shown in the specification but is derived from
   Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
   in Figure 2 of the specification (AAO30259)
CC CC
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC CC
SC Sequence 190 AA;

Query Match          97.2%; Score 1028; DB 7; Length 190;
Best Local Similarity 97.9%; Pred. No. 1,3e-86;
Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0

QY      1 QTTQPCTGTYNGFYFISYVNDGHGCVTYYNNGCGQFSYVMSNSGNFPGKGMCGTKNKVT 60
DB      1 QTTPGTGYNNGFYSYVNDGHGCVTYYNNGCGQFSYVMSNSGNFPGKGMOPETKNKVTL 60
QY      61 NFGSGYNPNKNSLSTLYVGSMRNPFLIEYIVENFGYVNPSTGATLGECTSDGSYYDIYRT 120
DB      61 NFGSGSYNPNKNSLSTLYVGMRSKPFLIEYIVENFGYVNPSTGATLGESVDSDGSYYDIYRT 120
QY      121 QRNVSPSIIGTAIFYVGVSVRRNRHSSGSVNTAHFNMAAQGLTGTMDOYIVAAGYF 180
DB      121 QRNVSPSIIGTAIFYVGVSVRRNRHSSGSVNTAHFNMAAQGLTGTMDOYIVAAGYF 180
QY      181 SSGSASITVS 190
DB      181 SSGSASITVS 190

```

RESULT 11

AAO30303
ID AAO30303 standard; protein; 190 AA.

XX AAO30303;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (Q161R).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.XX Hypocrea jecorina.
XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 161 /note= "Wild type Gln substituted with Arg"

XX MO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002MO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

XX MPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AAO30259)

XX Sequence 190 AA;

XX Query Match 97.1%; Score 1027; DB 7; Length 190;

XX Best Local Similarity 97.9%; Pred. No. 1.6e-86;

XX Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPTGYNNGYFYSYVNDGSGVYTNPGPGQFVSVMNSNGNFVGGKMGQPGTKNKVI 60

DB 1 QTIQPTGYNNGYFYSYVNDGSGVYTNPGPGQFVSVMNSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

DB 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

QY 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIVAVEGYF 180

DB 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190

DB 181 SSGSASITVS 190

RESULT 12

AAO30301
ID AAO30301 standard; protein; 190 AA.

XX AAO30301;

XX 03-SEP-2003 (first entry)

XX Trichoderma reesei xylanase II mutant protein (S75G).

XX Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.XX Hypocrea jecorina.
XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 75 /note= "Wild type Ser substituted with Gly"

XX MO2003046169-A2.

XX 05-JUN-2003.

XX 20-NOV-2002; 2002MO-CA001758.

XX 21-NOV-2001; 2001US-00990874.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

XX MPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.

XX Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermophilicity, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AAO30259)

XX Sequence 190 AA;

XX Query Match 97.1%; Score 1027; DB 7; Length 190;

XX Best Local Similarity 97.9%; Pred. No. 1.6e-86;

XX Matches 186; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPTGYNNGYFYSYVNDGSGVYTNPGPGQFVSVMNSNGNFVGGKMGQPGTKNKVI 60

DB 1 QTIQPTGYNNGYFYSYVNDGSGVYTNPGPGQFVSVMNSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

DB 61 NFSGSYNPNNGSYLSYVGMGRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

QY 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIVAVEGYF 180

DB 121 QRVNQPSTIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190

DB 181 SSGSASTIVS 190

RESULT 13

AA018647
ID AA018647 standard; protein; 190 AA.

XX AA018647;

DT 12-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

DE Trichoderma reesei xyn II xylanase.

XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;

XX Bleaching agent.

OS Hypocrea jecorina.

XX WO2000068396-A2.

PD 16-NOV-2000.

PF 12-MAY-2000; 2000WO-US013172.

PR 12-MAY-1999; 99US-0133714P.

XX (XENC-) XENCOR INC.

XX Bentzien J;

XX WPI; 2000-679800/66.

PT Non naturally occurring XA protein with enhanced thermostability,

PT alkalophilicity or thermostability relative to the naturally occurring

PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX Disclosure; Fig 16U; 114P; English.

CC The present sequence is given in a specification relating to non
CC naturally occurring xylanase activity (XA) proteins. The XA proteins
CC comprise an amino acid sequence less than 97% identical to a naturally
CC occurring Bacillus circulans xylanase. They are modified to exhibit
CC enhanced thermostability, alkalophilicity or thermostability relative to
CC the naturally occurring B. circulans xylanase. They may be used as the
CC active compound in a bleaching agent which is used for bleaching pulp.
CC (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 97.0%; Score 1026; DB 3; Length 190;

Best Local Similarity 98.4%; Pred. No. 2e-86;

Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTPGTCYNNNGYFYISYNDGHCYVYTNPGGQFSYVMSNSGTFVGGKMQPOTKXKYN 61

DB 2 TTPGTCYNNNGYFYISYNDGHCYVYTNPGGQFSYVMSNSGTFVGGKMQPOTKXKYN 61

QY 62 FSGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTVPSTGATKLGECTSDGSVYDIYRQ 121

DB 62 FSGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTVPSTGATKLGECTSDGSVYDIYRQ 121

QY 122 RVNOPSIIIGTATFYQYWSVRRNRSSGSVNTANHFMAAOGHLLGTMDYQIYAVEGYS 181

DB 122 RVNOPSIIIGTATFYQYWSVRRNRSSGSVNTANHFMAAOGHLLGTMDYQIYAVEGYS 181

QY 182 SSGSASTIVS 190

DB 182 SSGSASTIVS 190

RESULT 14

DB 181 SSGSASTIVS 190

AA018647

AA018647 standard; protein; 190 AA.

XX AA018647;

DT 29-AUG-2003 (revised)

DT 24-OCT-2002 (first entry)

DE T reesei xyn II xylanase.

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

XX liquid clarification; coffee extraction; plant oil extraction;

XX starch extraction; food thickener; animal food additive; mutant; mutein.

OS Hypocrea jecorina.

XX WO200238746-A2.

PD 16-MAY-2002.

PF 09-NOV-2001; 2001WO-US048018.

PR 10-NOV-2000; 2000US-00710050.

XX (XENC-) XENCOR INC.

XX Bentzien J, Dahiyat B;

XX WPI; 2002-608200/65.

PT Novel xylanase activity protein, useful in bleaching process of pulp and

PT in food and animal feed industry, has enhanced thermostability and

PT alkalophilicity.

XX Disclosure; Fig 16U; 121P; English.

CC The present invention relates to a non-naturally occurring xylanase
CC activity (XA) protein comprising an amino acid sequence less than 97%
CC identical to a naturally occurring Bacillus circulans xylanase, where the
CC protein has been modified to exhibit enhanced thermostability,
CC alkalophilicity, or thermostability relative to naturally occurring B.
CC circulans xylanase, and has at least 5 amino acid substitutions. A
CC bleaching agent comprising a modified xylanase is useful for bleaching
CC pulp, in the bioconversion of lignocellulosic materials to fuels, for
CC clarifying juice and wine, extracting coffee, plant oils and starch,
CC producing food thickener, altering texture in bakery products, e.g.
CC improving the quality of dough, helping bread to rise and processing of
CC wheat and corn for starch production, use as animal food additives to aid
CC in the digestibility of feedstuffs and in the washing of super precision
CC devices and semiconductors. The present sequence is a xylanase protein
CC described in the exemplification of the invention. (Updated on 29-AUG-
CC 2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 97.0%; Score 1026; DB 5; Length 190;

Best Local Similarity 98.4%; Pred. No. 2e-86;

Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTPGTCYNNNGYFYISYNDGHCYVYTNPGGQFSYVMSNSGTFVGGKMQPOTKXKYN 61

DB 2 TTPGTCYNNNGYFYISYNDGHCYVYTNPGGQFSYVMSNSGTFVGGKMQPOTKXKYN 61

QY 62 FSGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTVPSTGATKLGECTSDGSVYDIYRQ 121

DB 62 FSGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTVPSTGATKLGECTSDGSVYDIYRQ 121

QY 122 RVNOPSIIIGTATFYQYWSVRRNRSSGSVNTANHFMAAOGHLLGTMDYQIYAVEGYS 181

DB 122 RVNOPSIIIGTATFYQYWSVRRNRSSGSVNTANHFMAAOGHLLGTMDYQIYAVEGYS 181

QY 182 SSGSASTIVS 190

DB 182 SSGSASTIVS 190

Db 182 SGSASITVS 190

Db 181 SSGSASITVS 190

Search completed: August 17, 2004, 14:31:39
Job time : 54 secs

AC	AA030304	AA030304 standard; protein, 190 AA.
AC	AA030304	
DT	03-SEP-2003	(first entry)
DE	Trichoderma reesei xylanase II mutant protein (N11D).	
KW	xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;	
KW	pulp manufacture; poultry feed; swine feed; enzyme; mutant; muten.	
OS	Hypocrea jecorina.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 11	/note= "wild type Asn substituted with Asp"
FN	W02003046169-A2.	
PD	05-JUN-2003.	
PF	20-NOV-2002; 2002MO-CA001758.	
PR	21-NOV-2001; 2001US-00990874.	
XX	(CANADA) NAT RES COUNCIL CANADA.	
PI	Sung WL;	
DR	WPI; 2003-513647/48.	
PT	Novel modified xylanase useful in industrial process, exhibits improved	
PT	thermophilicity, alkalophilicity and expression efficiency, in comparison	
PT	to a corresponding native xylanase from Trichoderma reesei.	
XX	Example 1; Page: 105pp; English.	
XX	The invention relates to modified xylanase enzyme which exhibits improved	
CC	thermophilicity, alkalophilicity and expression efficiency, in comparison	
CC	to a corresponding native Trichoderma reesei xylanase (Trx). The modified	
CC	xylanase is useful in an industrial process e.g. pulp manufacturing. It	
CC	is useful for the bleaching of pulp, processing of precision devices and	
CC	for improving digestibility of poultry and swine feed. The present	
CC	sequence is Trichoderma reesei xylanase II mutant protein. Note: This	
CC	sequence is not shown in the specification but is derived from	
CC	Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16	
CC	in figure 2 of the specification (AA030259)	
XX		
SO	Sequence 190 AA;	
QY	Query Match	97.0%; Score 1026; DB 7; Length 190;
Db	Best Local Similarity	97.9%; Pred. No. 2e-86;
Db	Matches 186; Conservative 1; Mismatches 3; Indels 0; Gaps 0	
QY	1 OTTQPTGYNNGSYFVSYNNDHGAGVTYNNFGGQGFVSVMNSGPFVGGKMGGTNKKYI 60	
Db	1 OTTQPTGYNNDGTFYSYNNDDHGAGVTYNNFGGQGFVSVMNSGPFVGGKMGGTNKKYI 60	
QY	61 NFGSGYNPNGNSLYSVYGMNRPLLEYIVVENFGTINBSTGATLGGCTSDGSGVDIYRT 120	
Db	61 NFGSGYNPNGNSLYSVYGMNRPLLEYIVVENFGTINBSTGATLGGCTSDGSGVDIYRT 120	
QY	121 QRNVQSIIGTATFYVYVVRNRHSSGSVNTAHFNQMAOHGLLTGTMQYQVAVEGTF 180	
Db	121 QRNVQSIIGTATFYVYVVRNRHSSGSVNTAHFNQMAOHGLLTGTMQYQVAVEGTF 180	
QY	181 SSGSASITVS 190	

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Thu Aug 19 07:19:58 2004

us-09-856-025b-63.aug17.ra1

Page 1

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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:30:39 ; Search time 18 Seconds

(without alignments)
544.941 Million cell updates/sec

Title: US-09-856-025b-63

Perfect score: 1058

Sequence: 1 QTIQGTGYNNGYFYSYWNDD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6C.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	190	1	US-08-044-621D-26 Sequence 26, Appl
2	1031	97.4	190	1	US-08-709-912-16 Sequence 16, Appl
3	1031	97.4	190	2	US-09-047-370-16 Sequence 16, Appl
4	1031	97.4	223	2	US-08-121-436A-2 Sequence 2, Appl
5	1026	97.0	190	4	US-09-570-856B-22 Sequence 22, Appl
6	1021	96.5	190	4	US-08-709-912-17 Sequence 17, Appl
7	1021	96.5	190	2	US-09-047-370-17 Sequence 17, Appl
8	1018	96.2	190	1	US-08-044-621D-27 Sequence 27, Appl
9	1015	95.9	223	3	US-09-254-733-7 Sequence 19, Appl
10	1008	95.3	190	4	US-09-570-856B-19 Sequence 28, Appl
11	995	94.0	190	1	US-08-044-621D-28 Sequence 14, Appl
12	995	94.0	190	2	US-08-709-912-14 Sequence 14, Appl
13	995	94.0	190	2	US-09-047-370-14 Sequence 20, Appl
14	989	93.5	190	4	US-09-570-856B-20 Sequence 2, Appl
15	711.5	67.2	261	3	US-08-768-373-2 Sequence 2, Appl
16	711.5	67.2	261	4	US-09-849-242A-2 Sequence 26, Appl
17	666.5	63.0	225	4	US-09-570-856B-26 Sequence 8, Appl
18	655.5	62.0	225	1	US-08-290-979A-8 Sequence 4, Appl
19	649.5	61.4	230	3	US-08-768-373-4 Sequence 4, Appl
20	649.5	61.4	230	4	US-09-849-242A-4 Sequence 2, Appl
21	645	61.0	226	4	US-09-367-891A-2 Sequence 29, Appl
22	639.5	60.4	221	4	US-09-570-856B-29 Sequence 2, Appl
23	637.5	60.3	223	4	US-09-462-246-2 Sequence 2, Appl
24	625.5	59.1	225	2	US-08-886-765-2 Sequence 2, Appl
25	625.5	59.1	225	3	US-09-115-660-2 Sequence 4, Appl
26	623.5	58.9	227	1	US-08-458-023B-4 Sequence 24, Appl
27	620.5	58.6	194	4	US-09-570-856B-24

28	620	58.6	231	2	US-08-902-655A-6 Sequence 6, Appl
29	620	58.6	296	1	US-08-507-431-6 Sequence 6, Appl
30	620	58.6	296	3	US-09-116-622-6 Sequence 6, Appl
31	620	58.6	296	3	US-09-219-277-6 Sequence 6, Appl
32	620	58.6	296	3	US-09-599-661-6 Sequence 2, Appl
33	613.5	58.0	194	4	US-09-570-856B-23 Sequence 13, Appl
34	608.5	57.3	189	1	US-08-709-912-13 Sequence 13, Appl
35	606.5	57.3	189	2	US-09-047-370-13 Sequence 2, Appl
36	585.5	55.3	344	4	US-08-468-812-2 Sequence 2, Appl
37	585.5	55.3	344	2	US-08-530-563-2 Sequence 2, Appl
38	585.5	55.3	344	4	US-09-770-621-2 Sequence 2, Appl
39	585.5	55.3	344	4	US-09-235-832-2 Sequence 2, Appl
40	581	54.9	206	1	US-08-315-695-19 Sequence 19, Appl
41	581	54.9	215	1	US-08-044-621D-34 Sequence 34, Appl
42	581	54.9	335	4	US-09-570-856B-15 Sequence 10, Appl
43	579	54.7	191	2	US-08-709-912-10 Sequence 10, Appl
44	579	54.7	191	2	US-09-047-370-10 Sequence 10, Appl
45	555.5	52.5	197	1	US-08-044-621D-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-044-621D-26
Sequence 26, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yasuchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowling, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gudy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, Xyn II, 21kD, pl 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torionene, A., Mach, R.L., Messner, R.,
Gonzalez, R., Kalkkinen, N., Harkki, A.,
AUTHORS: & Kubicek, C.P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 97.4%; Score 1031; DB 1; Length 190;
Best Local Similarity 98.4%; Pred. No. 2.5e-89;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGFYYSYVNDGHCYVYTNNGPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60
DB 1 QTIQPGTYNNGFYYSYVNDGHCYVYTNNGPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSQSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSQSVYDIYRT 120
QY 121 QRVNPSIICTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNPSIICTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELEPHONE: (212) 758-2400
TELEPHONE: (212) 758-2962
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II

PUBLICATION INFORMATION:
AUTHORS: Torionene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 97.4%; Score 1031; DB 1; Length 190;
Best Local Similarity 98.4%; Pred. No. 2.5e-89;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGFYYSYVNDGHCYVYTNNGPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60
DB 1 QTIQPGTYNNGFYYSYVNDGHCYVYTNNGPGGQFSVWMSNGNFVGKGMQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSQSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGWSRNPLIEYIVENFGTYNPSTGATKLGCVTSQSVYDIYRT 120
QY 121 QRVNPSIICTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNPSIICTATFFQYWSVRNRHSSGSVNTANFNCAOGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSES: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039,2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2382
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
SPRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Tortorene, A
AUTHORS: Mach, R. U.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 97.4%; Score 1031; DB 2; Length 190;
Best Local Similarity 98.4%; Pred. No. 2,5e-89;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYVNDHGVTYNTGPGQFVSVMNSGNFVGKGMQPGTKXKVI 60
DB 1 QTIQGTGTNNGYFYSYVNDHGVTYNTGPGQFVSVMNSGNFVGKGMQPGTKXKVI 60
QY 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
DB 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Riitta
APPLICANT: Paloheimo, Marja
APPLICANT: Laitinen, Tarja
APPLICANT: Fagerstr m, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimballa, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 97.4%; Score 1031; DB 2; Length 223;
Best Local Similarity 98.4%; Pred. No. 3e-89;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYVNDHGVTYNTGPGQFVSVMNSGNFVGKGMQPGTKXKVI 60
DB 34 QTIQPGTYNNGYFYSYVNDHGVTYNTGPGQFVSVMNSGNFVGKGMQPGTKXKVI 93
QY 61 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
DB 94 NFSGSYPNNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 153
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 180
DB 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLTGTMDOYIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 5
US-09-570-856B-22

Sequence 22, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahiyat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-6/478-1/PFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/743,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 190
TYPE: PRP
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "pCa NH3+"
US-09-570-856B-22

Query Match 97.0%; Score 1026; DB 4; Length 190;
Best Local Similarity 98.4%; Pred. No. 7.3e-89;
Matches 186; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TTQPGTGNNGFFYYWMDHGCVTYTNGPGQGSVYVNSNGNPFVGGKMGPGTKNKYIN 61
DB 2 TTQPGTGNNGFFYYWMDHGCVTYTNGPGQGSVYVNSNGNPFVGGKMGPGTKNKYIN 61
QY 62 FPGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYIRTQ 121
DB 62 FPGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYIRTQ 121
QY 122 RVNOPSIIIGTATFYQWYVSRNRHSSGSVNTANHFNCACHGLTGLTMDYQIVAVEGYFS 181
DB 122 RVNOPSIIIGTATFYQWYVSRNRHSSGSVNTANHFNCACHGLTGLTMDYQIVAVEGYFS 181
QY 182 SSGSASITVS 190
DB 182 SSGSASITVS 190

RESULT 6
US-08-709-912-17
Sequence 17, Application US/08709912
Patent No. 575840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujie, M
AUTHORS: Watson, D. C.
AUTHORS: Wakarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992

US-08-709-912-17
Query Match 96.5%; Score 1021; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 2.1e-88;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGFFYYWMDHGCVTYTNGPGQGSVYVNSNGNPFVGGKMGPGTKNKYI 60
DB 1 QTIQPGTGNNGFFYYWMDHGCVTYTNGPGQGSVYVNSNGNPFVGGKMGPGTKNKYI 60
QY 61 NFGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYIRT 120
DB 61 NFGSYNPNNGNSLYSVGWSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYIRT 120
QY 121 QRVNOPSIIIGTATFYQWYVSRNRHSSGSVNTANHFNCACHGLTGLTMDYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQWYVSRNRHSSGSVNTANHFNCACHGLTGLTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

Page 5

	Query Match	Score 1021	DB 2	Length 190
	Best Local Similarity	97.4%	Pred. No. 2.1e-88	
Matches	185	Conservative	1	Mismatches 4; Indels 0; Gaps 0
QY	1	QTLPDPTGTYNNNGYFYSYNNDDHGVTYTYNNGPQGGQSVVMSNSGNFTVGGKMGWPGTKNKVYI	60	
Db	1	QTICPGTGFNNNGYFYSYNNDDHGVTYTYNNGPQGGQSVVMSNSGNFTVGGKMGWPGTKNKVYI	60	
QY	61	NFSGSYNNNGNSYLSVTVGMSRRLPLEEYIVENFGTYNPDSTGATKLGECSDSDSYVDIYRT	120	
Db	61	NFSGSYNNNGNSYLSVTVGMSRRLPLEEYIVENFGTYNPDSTGATKLGCVTSDSDSYVDIYRT	120	
QY	121	QRVNPSPSIIIGTATFYQYWSVRNRHNSSGSVNTAHNPNCAQHGTLTGIMDYQIVAVEGYF	180	
Db	121	QRVNPSPSIIIGTATFYQYWSVRNRHNSSGSVNTAHNPNCAQGLTLGIMDYQIVAVEGYF	180	
QY	181	SSGSASITVS	190	
Db	181	SSGSASITVS	190	

```

1 ADDRESSEE: Gowing, Strathy & Henderson
2 STREET: Suite 2600, 160 Elgin Street
3 CITY: Ottawa
4 STATE: Ontario
5 COUNTRY: Canada
6 ZIP: K1P 1C3
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
10 COMPUTER: IBM PC
11 OPERATING SYSTEM: PC-DOS
12 SOFTWARE: WordPerfect 5.1
13
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/044,621D
16 FILING DATE: April 8, 1993
17 CLASSIFICATION: 435
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER:
20 FILING DATE:
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Judy A. Erratt
23 REGISTRATION NUMBER: 34,076
24 REFERENCE/DOCKET NUMBER: 08-863796
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 613-786-0199
27 TELEFAX: 613-563-9869
28
29
30 INFORMATION FOR SEQ ID NO: 27:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 190
33 TYPE: Amino Acid
34 STRANDEDNESS: No. 5405769 Relevant
35 TOPOLOGY: linear
36 MOLECULE TYPE:
37 DESCRIPTION: protein
38 HYPOTHEICAL: No
39 ANTI-SENSE: No
40 FRAGMENT TYPE: No
41 ORIGINAL SOURCE:
42 ORGANISM: Trichoderma viride
43 STRAIN: Trichoderma viride, 20kD
44 IMMEDIATE SOURCE:
45 POSITION IN GENOME:
46 FEATURE:
47 PUBLICATION INFORMATION:
48 AUTHORS: Yasuchi M., Roy C., Ujile M., Watson
49 AUTHORS: D.C., & Wakarchuk W.
50 TITLE: Amino Acid Sequence of the Low-Molecular-
51 weight Xylanase from Trichoderma viride
52 JOURNAL: Xylans and Xylanases
53 VOLUME:
54 ISSUE:
55 PAGES: 145-154
56 DATE: 1992
57 DOCUMENT NUMBER:
58 FILING DATE:
59 PUBLICATION DATE:
60 RELEVANT RESIDUES IN SEQ ID NO:
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Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANFNMAAQGLTGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 9

US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ; GENERAL INFORMATION:
 ; APPLICANT: WATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORI
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: MURAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; TITLE OF INVENTION: PROTEINS OR PEPTIDES THEREWITH
 ; FILE REFERENCE: 99-0266*/LC(WMC)/00144
 ; CURRENT APPLICATION NUMBER: US/09/254,733
 ; CURRENT FILING DATE: 1999-05-07
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: TRICHODERMA VIRIDE MC300-1
 US-09-254-733-7

Query Match 95.9%; Score 1015; DB 3; Length 223;
 Best Local Similarity 96.3%; Pred. No. 9,7e-88;
 Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQGFSVNMSNGNFVGGKGMQPGTKNKVI 60
 Db 34 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQGFSVNMSNGNFVGGKGMQPGTKNKVI 93
 QY 61 NFSGSYNPNNGSYLTVYGWSRNPILYYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120
 Db 94 NFSGSYNPNNGSYLTVYGWSRNPILYYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 153
 QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANFNMAAQGLTGTMDYQIVAVEGYF 180
 Db 154 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANFNMAAQGLTGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 10

US-09-570-856B-19
 ; Sequence 19, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahiyat, Bassem I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/RFT/RMS/RMK
 ; CURRENT APPLICATION NUMBER: US/09/570,856B
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133,714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Trichoderma viride
 US-09-570-856B-19

Query Match 95.3%; Score 1008; DB 4; Length 190;
 Best Local Similarity 95.8%; Pred. No. 3,6e-87;
 Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQGFSVNMSNGNFVGGKGMQPGTKNKVI 60
 Db 1 QTIQPGTGYNNGYFYSYWMDGHGVTYTNPGGQGFSVNMSNGNFVGGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGSYLTVYGWSRNPILYYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120
 Db 61 NFSGSYNPNNGSYLTVYGWSRNPILYYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120
 QY 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANFNMAAQGLTGTMDYQIVAVEGYF 180
 Db 121 QRVNPSIIIGTATFYQYWSVRTRHSSGSVNTANFNMAAQGLTGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 11

US-08-044-621D-28
 ; Sequence 28, Application US/08044621D
 ; Patent No. 5405769
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren W. Makarchuk
 ; APPLICANT: Wing L. Sung
 ; APPLICANT: Makoto Yaguchi
 ; APPLICANT: Robert L. Campbell
 ; APPLICANT: David R. Rose
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 ; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gowing, Strachy & Henderson
 ; STREET: Suite 2600, 160 Elgin Street
 ; CITY: Ottawa
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: K1P 1C3
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/044,621D
 ; FILING DATE: April 8, 1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Judy A. Erratt
 ; REGISTRATION NUMBER: 34,076
 ; REFERENCE/DOCKET NUMBER: 08-863796
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 613-786-0199
 ; TELEFAX: 613-563-9869
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 190
 ; TYPE: Amino Acid
 ; STRANDEDNESS: No, 5405769 Relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: No
 ; ANTI-SENSE: No
 ; FRAGMENT TYPE: NO
 ; ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match
Best Local Similarity 94.0%; Score 995; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 5,9e-86;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNNGFYSTYNDGAGVYTYNNGPGGQFSYVMSNSGNFVGKGMQGTAKVI 60
DB 1 OTTGTGTYNNNGFYSTYNDGAGVYTYNNGPGGQFSYVMSNSGNFVGKGMQGTAKVI 60

QY 61 NFSGSYVNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
DB 61 NFSGSYVNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120

QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNCMAQHGTLGTMDYQIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNCMAQHGTLGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 12
US-08-709-912-14
Sequence 14, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/709,912
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oisen Mr. Warren E
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-08-709-912-14

Query Match
Best Local Similarity 94.0%; Score 995; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 5,9e-86;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNNGFYSTYNDGAGVYTYNNGPGGQFSYVMSNSGNFVGKGMQGTAKVI 60
DB 1 OTTGTGTYNNNGFYSTYNDGAGVYTYNNGPGGQFSYVMSNSGNFVGKGMQGTAKVI 60

QY 61 NFSGSYVNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
DB 61 NFSGSYVNPNGNSYLSYVGMGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120

QY 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNCMAQHGTLGTMDYQIVAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYVSVRRNRSSGSVNTANHFNCMAQHGTLGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 13
US-09-047-370-14
Sequence 14, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen M, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: internal
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Ten, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match 94.0%; Score 995; DB 2; Length 190;
Best Local Similarity 94.2%; Pred. No. 5,9e-86;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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DB 1 OTTGGTGNNGYFYVNDGAGVYTNNGPGGQFVNMNSGNFVGGKQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATKLGECTSDGSYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATKLGECTSDGSYDIYRT 120
QY 121 QRVNPSITIGTATFYQYVSVRRNHRSSGSVNTANFNCAOHGLTIGTMDYQIVAVEGYF 180
DB 121 QRVNPSITIGTATFYQYVSVRRNHRSSGSVNTANFNCAOHGLTIGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Benizien, Joerg M
APPLICANT: Dahlyac, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570,856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714

PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

Query Match 93.5%; Score 989; DB 4; Length 190;
Best Local Similarity 93.7%; Pred. No. 2.2e-85;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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QY 61 NFSGSYNPNNGSYLSYVGMNRNPLIEYIVENFGTNPSTGATKLGECTSDGSYDIYRT 120
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QY 121 QRVNPSITIGTATFYQYVSVRRNHRSSGSVNTANFNCAOHGLTIGTMDYQIVAVEGYF 180
DB 121 QRVNPSITIGTATFYQYVSVRRNHRSSGSVNTANFNCAOHGLTIGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHIMO, MARJA
APPLICANT: HAROLA, SATU
APPLICANT: M NYL, ARJA
APPLICANT: VERMAANPER, JARI
APPLICANT: LANTTO, RAIJA
APPLICANT: LAHTINEN, TARJA
APPLICANT: PAGERSTR, M, RICHARD
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMBALA, MICHAEL A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0540003
TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= X1NA
US-08-768-373-2

Query Match 67.2%; Score 711.5; DB 3; Length 261;
Best Local Similarity 64.7%; Pred. No. 3.8e-59;
Matches 123; Conservative 28; Mismatches 38; Indels 1; Gaps 1;

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Db 27 QTLTSSATGTNGYYISFWTDQGNIRFNLBSGGQSVTWSGNGMWVGKGNPQTDNRV 86
QY 60 INFSGSYNPNNGNSYLSVYGMNRNPLIEYIYVENFGTYNPSGTATKLGECTSPDGSYDIYR 119
Db 87 INVTADYRPNNGSYLAIVGWTNRPLEIYVVSFGTYDPSTGATRMGSVTTDGGTYNIYR 146
QY 120 TORVNOPSIIGTATFYQYVSFRNRHSSGSVNTANHFNCWAQHGILGTMDYQIVAVEGY 179
Db 147 TORVNAFPIEGTKTFYQYVSFRTSKRTGGTVTMANHFNAFRQAGLQLGSHDYQIVATEGY 206
QY 180 FSSGSASTIV 189
Db 207 YSSGSATVNV 216

Search completed: August 17, 2004, 14:33:51
Job time : 19 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: August 17, 2004, 14:32:59 ; Search time 46 Seconds
(without alignments)
1296.656 Million cell updates/sec

Title: US-09-856-025b-63

Perfect score: 1058
Sequence: 1 QTIQPGTGYNNGYFYSSYND.....YQIVAEYGFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	190	US-10-307-441-16	Sequence 16, Appl
2	1031	97.4	222	US-10-237-386-32	Sequence 32, Appl
3	1031	97.4	223	US-10-237-386-31	Sequence 31, Appl
4	1021	96.5	190	US-10-307-441-17	Sequence 17, Appl
5	1019	96.3	223	US-10-237-386-30	Sequence 30, Appl
6	995	94.0	190	US-10-307-441-14	Sequence 14, Appl
7	989	93.5	190	US-10-237-386-33	Sequence 33, Appl
8	866	81.9	223	US-10-237-386-34	Sequence 34, Appl
9	755.5	71.4	241	US-10-237-386-35	Sequence 35, Appl
10	698.5	63.8	219	US-10-237-386-29	Sequence 29, Appl
11	675	63.3	313	US-10-213-990-72	Sequence 72, Appl
12	669.5	63.3	227	US-10-237-386-22	Sequence 22, Appl
13	667.5	63.1	227	US-10-237-386-21	Sequence 21, Appl
14	665.5	62.9	234	US-10-213-990-69	Sequence 69, Appl
15	661.5	62.5	189	US-10-307-441-19	Sequence 19, Appl

16	659.5	62.3	221	US-10-213-990-66	Sequence 66, Appl
17	654.5	61.9	225	US-10-237-386-36	Sequence 36, Appl
18	646	61.1	221	US-10-237-386-37	Sequence 37, Appl
19	639.5	60.4	221	US-10-237-386-20	Sequence 20, Appl
20	637.5	60.3	223	US-10-237-386-2	Sequence 2, Appl
21	637	60.2	217	US-09-790-070A-11	Sequence 11, Appl
22	633.5	59.9	231	US-10-237-386-26	Sequence 26, Appl
23	626.5	59.2	231	US-10-237-386-25	Sequence 25, Appl
24	625.5	59.1	194	US-10-307-441-20	Sequence 20, Appl
25	625.5	59.1	225	US-09-467-368-2	Sequence 2, Appl
26	625.5	59.1	225	US-10-237-386-24	Sequence 24, Appl
27	619.5	58.6	221	US-10-237-386-44	Sequence 44, Appl
28	617.5	58.4	227	US-10-237-386-27	Sequence 27, Appl
29	608.5	57.5	239	US-10-237-386-40	Sequence 40, Appl
30	607.5	57.4	241	US-10-237-386-43	Sequence 43, Appl
31	606.5	57.3	189	US-10-307-441-13	Sequence 13, Appl
32	606.5	57.3	240	US-10-237-386-42	Sequence 42, Appl
33	592	56.0	228	US-10-237-386-39	Sequence 39, Appl
34	586	55.4	216	US-10-237-386-45	Sequence 45, Appl
35	585.5	55.3	344	US-09-770-621-2	Sequence 2, Appl
36	585.5	55.3	344	US-10-286-993-2	Sequence 2, Appl
37	583.5	55.2	242	US-10-237-386-41	Sequence 41, Appl
38	579	54.7	191	US-10-307-441-10	Sequence 10, Appl
39	564.5	53.4	233	US-10-237-386-28	Sequence 28, Appl
40	555.5	52.5	197	US-10-307-441-9	Sequence 9, Appl
41	555.5	52.5	201	US-10-237-386-23	Sequence 23, Appl
42	533.5	50.4	237	US-10-237-386-46	Sequence 46, Appl
43	523.5	49.5	236	US-10-237-386-47	Sequence 47, Appl
44	517.5	48.9	189	US-10-307-441-12	Sequence 12, Appl
45	517.5	48.9	226	US-10-237-386-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1
US-10-307-441-16
Sequence 16, Application US/10307441
Publication NO. US20030166236A1
GENERAL INFORMATION:
APPLICANT: SUNG, Wing J.
TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity
FILE REFERENCE: 027367-5006US
CURRENT APPLICATION NUMBER: US/10/307,441
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/213,803
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentm Ver. 2.1
SEQ ID NO 16
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma reesei
US-10-307-441-16

Query Match 97.4%; Score 1031; DB 14; Length 190;
Best Local Similarity 98.4%; Pred. No. 1,4e-92;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSSYNDHGCVTYTNGPGGQFSVWMSNGNFGVGKMGQGTCKKVI 60
Db 1 QTIQPGTGYNNGYFYSSYNDHGCVTYTNGPGGQFSVWMSNGNFGVGKMGQGTCKKVI 60
QY 61 NFSGSYNPNNGNSYISVVGWRNPLIEYIYENFGTYNPSTGATKLGBCISDGSVDIYRT 120
Db 61 NFSGSYNPNNGNSYISVVGWRNPLIEYIYENFGTYNPSTGATKLGBCISDGSVDIYRT 120
QY 61 NFSGSYNPNNGNSYISVVGWRNPLIEYIYENFGTYNPSTGATKLGBCISDGSVDIYRT 120
Db 61 NFSGSYNPNNGNSYISVVGWRNPLIEYIYENFGTYNPSTGATKLGBCISDGSVDIYRT 120
QY 121 QRVNPSIIIGATFYQYVSRNRHRSGSVNTANHFVCMQHGTLTGTMQYQIVAEVGF 180
Db 121 QRVNPSIIIGATFYQYVSRNRHRSGSVNTANHFVCMQHGTLTGTMQYQIVAEVGF 180

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Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMQYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 2
US-10-237-386-32
; Sequence 32, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-32

Query Match
Best Local Similarity 97.4%; Score 1031; DB 14; Length 222;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYVNDGHGVTYTNPGQGFVSVMNSNGNFVGKGMQPGTKNKVI 60
Db 33 QTIQPGTGYNNGYFYSYVNDGHGVTYTNPGQGFVSVMNSNGNFVGKGMQPGTKNKVI 92
QY 61 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
Db 93 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 152
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLGTMQYIVAVEGYF 180
Db 153 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMQYIVAVEGYF 212
QY 181 SSGSASITVS 190
Db 213 SSGSASITVS 222

RESULT 3
US-10-237-386-31
; Sequence 31, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-31

Query Match
Best Local Similarity 97.4%; Score 1031; DB 14; Length 223;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 61 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
Db 94 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 153
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLGTMQYIVAVEGYF 180
Db 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMQYIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 4
US-10-307-441-17
; Sequence 17, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Ming L.
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma viride
US-10-307-441-17

Query Match
Best Local Similarity 96.5%; Score 1021; DB 14; Length 190;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYVNDGHGVTYTNPGQGFVSVMNSNGNFVGKGMQPGTKNKVI 60
Db 1 QTIQPGTGYNNGYFYSYVNDGHGVTYTNPGQGFVSVMNSNGNFVGKGMQPGTKNKVI 60
QY 61 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
Db 61 NFGSYNPNNGNSLYSYGMSRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGTLGTMQYIVAVEGYF 180
Db 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMQYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190
```

RESULT 5
US-10-237-386-30
; Sequence 30, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRF
; ORGANISM: T. reesei
US-10-237-386-30

Query Match
Best Local Similarity 96.3%; Score 1019; DB 14; Length 223;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 60
DB 34 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 93
QY 61 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
DB 94 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 153
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180
DB 154 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 6
US-10-307-441-14
; Sequence 14, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Ming L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 190
; TYPE: PRF
; ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match
Best Local Similarity 94.0%; Score 995; DB 14; Length 190;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 60
DB 1 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 60
QY 61 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-10-237-386-33
; Sequence 33, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRF
; ORGANISM: T. harzianum
US-10-237-386-33

Query Match
Best Local Similarity 93.5%; Score 989; DB 14; Length 190;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 60
DB 1 OTTQPGTGNNGYFYSYWMDGHGVTYTNPGGQFSYVMSNSGNFVGKGMQGTNKKVI 60
QY 61 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVWGRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVYDIYRT 120
QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSGVNTANHFNCMAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8
US-10-237-386-34
; Sequence 34, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sidsesen, Ole

```
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237.386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 223
TYPE: PRT
ORGANISM: T. viride
US-10-237-386-34

Query Match      81.9%; Score 866; DB 14; Length 223;
Best Local Similarity 81.1%; Pred. No. 2,2e-76;
Matches 154; Conservative 12; Mismatches 24; Indels 0; Gaps 0;

QY 1 QTIQGTGYNNGYFYSYNDHGGVYTTNGPGGQSVVWMSNGNFVGGKMGQPTKRVYI 60
DB 34 QTIQGTGYNNGYFYSYNDHGGVYTTNGAGGSFVWMSNGNFVGGKMGNPSSSRVI 93
QY 61 NNSGYNPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 120
DB 94 NNSGYNPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRT 153
QY 121 QRVNPSITIGTATFYQVWSVRNRHSSGSVNTAHFNCAQHGLTLGMDYQIYAVBGYF 180
DB 154 QRVNPSITIGTATFYQVWSVRNRHAPARSRLRTTSNMRMLGLTLGMDYQIYAVBGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGNANINVS 223

RESULT 9
US-10-237-386-35
Sequence 35, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237.386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 241
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-35

Query Match      71.4%; Score 755.5; DB 14; Length 241;
Best Local Similarity 72.7%; Pred. No. 1.5e-65;
Matches 133; Conservative 21; Mismatches 28; Indels 1; Gaps 1;
```

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QY 67 NPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRTQVNP 126
DB 97 NPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRTQVNP 156
QY 127 SIIGTATFYQVWSVRNRHSSGSVNTAHFNCAQHGLTLGMDYQIYAVBGYFSSGAS 186
DB 157 SIIGTATFYQVWSVRNRHSSGSVNTAHFNCAQHGLTLGMDYQIYAVBGYFSSGAS 216
QY 187 ITV 189
DB 217 VNV 219

RESULT 10
US-10-237-386-29
Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237.386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 219
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-29

Query Match      65.8%; Score 696.5; DB 14; Length 219;
Best Local Similarity 67.6%; Pred. No. 7.7e-60;
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GGTGNNGYFYSYNDHGGVYTTNGPGGQSVVWMSNGNFVGGKMGQPTKRVYI 65
DB 36 GGTGNNGYFYSYNDHGGVYTTNGAGGSFVWMSNGNFVGGKMGNPSSSRVI 94
QY 66 YNPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRTQVNP 125
DB 95 YNPNNGSYLVYGMNRPLIEYIVENFGTYNPGTATKLGECTSDGSVYDIYRTQVNP 154
QY 126 PSITIGTATFYQVWSVRNRHSSGSVNTAHFNCAQHGLTLGMDYQIYAVBGYFSSGAS 185
DB 155 PSITIGTATFYQVWSVRNRHSSGSVNTAHFNCAQHGLTLGMDYQIYAVBGYFSSGAS 214
QY 186 SITVS 190
DB 215 SITVS 219

RESULT 11
US-10-213-990-72
Sequence 72, Application US/10213990
Publication No. US20030082555A1
GENERAL INFORMATION:
APPLICANT: Uiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
FILE REFERENCE: 10182-019-999
```


;/ CURRENT APPLICATION NUMBER: US/10/213,990
;/ CURRENT FILING DATE: 2002-08-05
;/ NUMBER OF SEQ ID NOS: 72
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 72
;/ LENGTH: 313
;/ TYPE: PRF
;/ ORGANISM: Aspergillus
US-10-213-990-72

Query Match 63.8%; Score 675; DB 14; Length 313;
Best Local Similarity 63.2%; Pred. No. 1.5e-57;
Matches 122; Conservative 29; Mismatches 38; Indels 4; Gaps 3;

QY 1 OTIQPG-TGNNGYEFYSYNNDDHGGVYTNNGPGGQFYSVWMS--NSGNFVGKGMQPGTKN 57
DB 32 QTTTTSQITGNNGYISFTWNGAGSYVWMAQNGGDFTCGKMNPGSDH 91
QY 58 KYINFGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPGTGATKLGECTSDGSVYDI 117
DB 92 D-ITFSGSFNPGSNALISVYGWTPNPLVEYILENVGSGYNPGSGMTHKGTVTSDDSTYDI 150
QY 118 YRTQKVNOSIIGTATFYQWVSRRHRSSGSVNTANHFNCMAQHGILGTMDYQIVAVE 177
DB 151 YEHQVNPISIVGTATFNQYWSIRONKRSSGTVTTANHFKAWASLGMNLGTHNYQIVASTE 210
QY 178 GFSSGSASITVS 190
DB 211 GYESSGTSITIVS 223

RESULT 12
US-10-237-386-22
;/ Sequence 22, Application US/10237386
;/ Publication No. US20030180895A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Danisco A/S
;/ APPLICANT: Sidsesen, Ole
;/ APPLICANT: Sorensen, Jens
;/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
;/ FILE REFERENCE: 674509-2046
;/ CURRENT APPLICATION NUMBER: US/10/237,386
;/ CURRENT FILING DATE: 2002-12-06
;/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
;/ PRIOR FILING DATE: 2001-03-08
;/ PRIOR APPLICATION NUMBER: GB 0005585.5
;/ PRIOR FILING DATE: 2000-03-08
;/ PRIOR APPLICATION NUMBER: GB 0015751.1
;/ PRIOR FILING DATE: 2000-06-27
;/ NUMBER OF SEQ ID NOS: 66
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 22
;/ LENGTH: 227
;/ TYPE: PRF
;/ ORGANISM: A. pisi
US-10-237-386-22

Query Match 63.3%; Score 669.5; DB 14; Length 227;
Best Local Similarity 64.2%; Pred. No. 3.5e-57;
Matches 124; Conservative 21; Mismatches 43; Indels 5; Gaps 2;

QY 2 TIOPG---GNNNGYFYSYNNDDHGGVYTNNGPGGQFYSVWMSNPNFVGKGMQPGTKN 57
DB 34 TPAAGTPSSQGTNNGCYFYSWTDGGAQATYTNAGAGSYVMKGTGNLVGKGMNPGAA- 92
QY 58 KYINFGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPGTGATKLGECTSDGSVYDI 117
DB 93 RTIYSGTSPSGNSYLAIVGWRNPLIYVVENFGTYNPGTGATKLGECTSDGSVYDI 152
QY 118 YRTQKVNOSIIGTATFYQWVSRRHRSSGSVNTANHFNCMAQHGILGTMDYQIVAVE 177
DB 153 AQTRTNPISIDTQTFQYWSIRONKRSSGSVNMKTHFDMAAKGMKLGTHNYQIVASTE 212

QY 178 GFSSGSASITVS 190
DB 213 GYSSGSASITVN 225

RESULT 13
US-10-237-386-21
;/ Sequence 21, Application US/10237386
;/ Publication No. US20030180895A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Danisco A/S
;/ APPLICANT: Sidsesen, Ole
;/ APPLICANT: Sorensen, Jens
;/ TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
;/ FILE REFERENCE: 674509-2046
;/ CURRENT APPLICATION NUMBER: US/10/237,386
;/ CURRENT FILING DATE: 2002-12-06
;/ PRIOR APPLICATION NUMBER: PCT/IB01/00426
;/ PRIOR FILING DATE: 2001-03-08
;/ PRIOR APPLICATION NUMBER: GB 0005585.5
;/ PRIOR FILING DATE: 2000-03-08
;/ PRIOR APPLICATION NUMBER: GB 0015751.1
;/ PRIOR FILING DATE: 2000-06-27
;/ NUMBER OF SEQ ID NOS: 66
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 21
;/ LENGTH: 227
;/ TYPE: PRF
;/ ORGANISM: H. turcicum
US-10-237-386-21

Query Match 63.1%; Score 667.5; DB 14; Length 227;
Best Local Similarity 63.7%; Pred. No. 5.5e-57;
Matches 121; Conservative 22; Mismatches 46; Indels 1; Gaps 1;

QY 1 OTIQPGTGNNGYFYSYNNDDHGGVYTNNGPGGQFYSVWMSNPNFVGKGMQPGTKN 60
DB 37 QSTNPGEGTNGCYFYSWTDGGAQATYTNAGAGSYVWTDGTLVGGKMNPGTA-RTI 95
QY 61 NFSGSYNPNNGNSYLSVYGWSRNPLEYIYVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120
DB 96 TYSQVNPNGNSYLAIVGWRNPLIYVVENFGTYNPGTGATKLGECTSDGSVYDIYRT 155
QY 121 ORVNPISIGTATFYQWVSRRHRSSGSVNTANHFNCMAQHGILGTMDYQIVAVEGYF 180
DB 156 TRIQPISIDTQTFQYWSIRONKRSSGSVNMKTHFDMAAKGMKLGTHNYQIVATEGYF 215
QY 181 SSGSASITVS 190
DB 216 SSGSASITVN 225

RESULT 14
US-10-213-990-69
;/ Sequence 69, Application US/10213990
;/ Publication No. US20030082595A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Jiang, Bo
;/ APPLICANT: Bussey, Howard
;/ APPLICANT: Storms, Reg
;/ APPLICANT: Roemer, Terry
;/ TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
;/ FILE REFERENCE: 10182-019-999
;/ CURRENT APPLICATION NUMBER: US/10/213,990
;/ CURRENT FILING DATE: 2002-08-05
;/ NUMBER OF SEQ ID NOS: 72
;/ SOFTWARE: FastSeq for Windows Version 4.0
;/ SEQ ID NO 69
;/ LENGTH: 234
;/ TYPE: PRF
;/ ORGANISM: Aspergillus
US-10-213-990-69

Thu Aug 19 07:19:59 2004

us-09-856-025b-63.aug17.rpr

Page 1

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:29:43 ; Search time 16 Seconds
(without alignments)
1142.274 Million cell updates/sec

Title: US-09-856-025B-63
Perfect score: 1058
Sequence: 1 QTIQPGTGYNNNGYFYSSYVND.....YQIVAVGEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir78:*
2: pir71:*
3: pir72:*
4: pir73:*
5: pir74:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1031	97.4	222	2	S39154 xylanase 1 - fungus
2	1031	97.4	223	2	S39883 endo-1,4-beta-xylo
3	1008	95.3	190	1	A44594 endo-1,4-beta-xylo
4	1004	94.9	190	1	A44595 endo-1,4-beta-xylo
5	995	94.0	190	1	A44593 endo-1,4-beta-xylo
6	755.5	91.4	241	2	S71473 endo-1,4-beta-xylo
7	698.5	63.8	219	2	S71472 endo-1,4-beta-xylo
8	695.5	63.7	232	2	UC7577 endo-1,4-beta-xylo
9	674.5	63.8	225	1	S57477 endo-1,4-beta-xylo
10	663.5	62.7	221	1	S57469 endo-1,4-beta-xylo
11	646	61.1	221	2	UC7307 endo-1,4-beta-xylo
12	617.5	58.4	227	2	S43919 endo-1,4-beta-xylo
13	581	54.9	323	1	JS0591 endo-1,4-beta-xylo
14	581	54.9	335	2	TS0601 endo-1,4-beta-xylo
15	564.5	53.4	644	1	I40712 endo-1,4-beta-xylo
16	555.5	52.5	197	1	A44597 endo-1,4-beta-xylo
17	533.5	50.4	661	1	S59633 endo-1,4-beta-xylo
18	523.5	49.5	656	1	S59631 endo-1,4-beta-xylo
19	520.5	49.2	241	2	T37005 endo-1,4-beta-xylo
20	517	48.9	240	1	JS0591 endo-1,4-beta-xylo
21	515	48.7	240	1	S47512 endo-1,4-beta-xylo
22	514.5	48.6	210	2	C83762 endo-1,4-beta-xylo
23	502	47.4	213	1	I40569 endo-1,4-beta-xylo
24	501	47.4	213	1	S01734 endo-1,4-beta-xylo
25	501	47.4	213	1	S48126 endo-1,4-beta-xylo
26	459	43.3	354	1	S51779 endo-1,4-beta-xylo
27	458	43.3	354	1	MMBSXP endo-1,4-beta-xylo
28	443.5	41.9	261	1	S12745 endo-1,4-beta-xylo
29	436.5	41.3	209	2	JC4909 endo-1,4-beta-xylo

30	436	41.2	511	1	QJ1935 endo-1,4-beta-xylo
31	433	40.9	211	1	S48229 endo-1,4-beta-xylo
32	432.5	40.9	229	2	S39155 xylanase 2 - fungus
33	431	40.7	211	2	S49542 endo-1,4-beta-xylo
34	428	40.5	211	1	TC1198 endo-1,4-beta-xylo
35	392	37.1	954	1	S20507 endo-1,4-beta-xylo
36	384	36.3	789	2	S58235 endo-1,4-beta-xylo
37	377.5	35.7	802	2	A36910 xylanase, beta(1,3
38	370	35.0	781	2	S51592 xynB precursor - R
39	294	27.8	607	2	S49528 endoxylnase - rum
40	294	27.8	607	2	S24754 endo-1,4-beta-xylo
41	282.5	26.7	608	2	B53295 xylanase (EC 3.2.1
42	280	26.5	50	2	A61149 endo-1,4-beta-xylo
43	237.5	22.4	266	1	S48865 endo-1,4-beta-xylo
44	119.5	11.3	1053	2	B70987 probable PEP prote
45	118	11.2	2817	2	B97033 uncharacterized pr

ALIGNMENTS

```
RESULT 1
S39154
xylanase 1 - fungus (Trichoderma reesei)
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C:Accession: S39154
R:Roercken, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkkinen, N.; Harkki, A.; Kubi
Biotechnology 10, 1461-1465, 1992
A:Title: The two major xylanases from trichoderma reesei: characterization of both enzym
A:Reference number: S39154
A:Accession: S39154
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <TOE>
A:Cross-references: EMBL:X69573; NID:g396563; PID:CAA49293.1; PID:g396564
C:Genetics:
A:Gene: xyn1
A:Introns: 90/2
F:44-222/Domain: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
F:44-222/Domain: endo-1,4-beta-xylanase homology <XYL>

Query Match          97.4%; Score 1031; DB 2; Length 222;
Best local similarity 98.4%; Pred. No. 2,3e-73;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSSYVNDHGCVYTYNGPGQPSYVMSNSGNFVGKQWQPTKKVI 60
    1031 97.4 223 2 S39883 endo-1,4-beta-xylo
    1008 95.3 190 1 A44594 endo-1,4-beta-xylo
    1004 94.9 190 1 A44595 endo-1,4-beta-xylo
    995 94.0 190 1 A44593 endo-1,4-beta-xylo
    755.5 91.4 241 2 S71473 endo-1,4-beta-xylo
    698.5 63.8 219 2 S71472 endo-1,4-beta-xylo
    695.5 63.7 232 2 UC7577 endo-1,4-beta-xylo
    674.5 63.8 225 1 S57477 endo-1,4-beta-xylo
    663.5 62.7 221 1 S57469 endo-1,4-beta-xylo
    646 61.1 221 2 UC7307 endo-1,4-beta-xylo
    617.5 58.4 227 2 S43919 endo-1,4-beta-xylo
    581 54.9 323 1 JS0591 endo-1,4-beta-xylo
    581 54.9 335 2 TS0601 endo-1,4-beta-xylo
    564.5 53.4 644 1 I40712 endo-1,4-beta-xylo
    555.5 52.5 197 1 A44597 endo-1,4-beta-xylo
    533.5 50.4 661 1 S59633 endo-1,4-beta-xylo
    523.5 49.5 656 1 S59631 endo-1,4-beta-xylo
    520.5 49.2 241 2 T37005 endo-1,4-beta-xylo
    517 48.9 240 1 JS0591 endo-1,4-beta-xylo
    515 48.7 240 1 S47512 endo-1,4-beta-xylo
    514.5 48.6 210 2 C83762 endo-1,4-beta-xylo
    502 47.4 213 1 I40569 endo-1,4-beta-xylo
    501 47.4 213 1 S01734 endo-1,4-beta-xylo
    501 47.4 213 1 S48126 endo-1,4-beta-xylo
    459 43.3 354 1 S51779 endo-1,4-beta-xylo
    458 43.3 354 1 MMBSXP endo-1,4-beta-xylo
    443.5 41.9 261 1 S12745 endo-1,4-beta-xylo
    436.5 41.3 209 2 JC4909 endo-1,4-beta-xylo

Db 33 QTIQPGTGYNNNGYFYSSYVNDHGCVYTYNGPGQPSYVMSNSGNFVGKQWQPTKKVI 92
    61 NFGSYNPNNGSYLYSVYVWGSNPLIEYIVENFTYVPSGATKLGCTSDGSYYDIYRT 120
    93 NFGSYNPNNGSYLYSVYVWGSNPLIEYIVENFTYVPSGATKLGCTSDGSYYDIYRT 152
    121 QVNVPSIIIGATFYQVSVVRNRRSSGSVNTANHFNCMAQHGLITGMDYQIVAVEGYF 180
    153 QVNVPSIIIGATFYQVSVVRNRRSSGSVNTANHFNCMAQHGLITGMDYQIVAVEGYF 212
    181 SSGSASITVS 190
    213 SSGSASITVS 222

QY 181 SSGSASITVS 190
    213 SSGSASITVS 222

Db 181 SSGSASITVS 190
    213 SSGSASITVS 222

RESULT 2
S39883
endo-1,4-beta-xylanase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N:Alternate names: endoxylnase II
C:Species: Trichoderma reesei
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S39883; S39884
R:Saarelainen, R.; Paloheimo, M.; Fagerstrom, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A:Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylnar
```

A:Reference number: S39883; MUID:94088442; PMID:8264524
A:Accession: S39883
A:Molecule type: DNA
A:Residues: 1-223 <SAA>
A:Cross-References: EMBL:567387; NID:9455906; PID:AA29346.1; PID:9455907
A:Experimental source: strain QM6a
A:Accession: S39884
A:Molecule type: protein
A:Residues: 34-43,49-57,121-151,178-191 <SAF>
A:Genetics:
A:Gene: xln2
A:Introns: 91/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
F:1-15/Domain: signal sequence #status predicted <SIG>
F:20-33/Domain: signal sequence #status predicted <PRO>
F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
F:45-223/Product: endo-1,4-beta-xylanase homology <XLY>
F:11,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:110,121/Binding site: substrate (Tyr) #status predicted
F:119,210/Active site: Glu #status predicted

Query Match 97.4%; Score 1031; DB 2; Length 223;
Best Local Similarity 98.4%; Pred. No. 2,3e-73;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 60
DB 34 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 93

QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 120
DB 94 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 153

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 180
DB 154 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 213

QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 3
A44594
endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
N:Alternate names: xylanase IIA
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
C:Accession: A44594
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44594
A:Molecule type: protein
A:Residues: 1-190 <YAG>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XLY>
F:177,88/Binding site: substrate (Tyr) #status predicted
F:86,177/Active site: Glu #status predicted

Query Match 95.3%; Score 1008; DB 1; Length 190;
Best Local Similarity 95.8%; Pred. No. 1,2e-71;
Matches 182; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 60

DB 1 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
A44595
endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma vir
N:Alternate names: xylanase IIB
C:Species: Trichoderma viride
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
C:Accession: A44595
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44595
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-190 <YAG>
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:12-190/Domain: endo-1,4-beta-xylanase homology <XLY>
F:86,177/Active site: Glu #status predicted
F:126-127/Cleavage site: Pro-ser (unidentified proteinase) #status predicted
F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 94.9%; Score 1004; DB 1; Length 190;
Best Local Similarity 95.3%; Pred. No. 2,5e-71;
Matches 181; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 60
DB 1 QTIQGTGNNNGFYFYSYNDHGGVYTYTNGPGQGSVWMSNGNFVGGKMGQPGTKNKVI 60

QY 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGWSRNPLIEYIVENFGTYNPSTGATKLGECTSDGSVDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 180
DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNCMAHQGLTLGTMDOIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 5
A44593
endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain
N:Alternate names: xylanase
C:Species: Trichoderma harzianum
C:Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
C:Accession: A44593
R:Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A:Reference number: A44593
A:Accession: A44593
A:Molecule type: protein

A/Accession: PC7086
A/Molecule type: protein
A/Residues: 32-51 <K12>
C/Genetics:
A/Gene: xylA
A/Introns: 89/2
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycoprotein; glycosidase; hydrolase

Query Match 51.1%; Score 646; DB 2; Length 221;
Best Local Similarity 60.7%; Pred. No. 2,3e-43;
Matches 116; Conservative 30; Mismatches 43; Indels 2; Gaps 2;

QY 1 CTIQPG-TGYNNGFYSYWMDHGQVYTYNPGQGFVSVMNSGNGFVGKGMQPTKXKV 59
|||
DB 32 CTTSSQGTNNNGYYSFWTNGGTVQYTNCAAGESVTWENCGDFTSGKGMSTGSA-RD 90
|||
QY 60 INFSGSYNPNNGSYVYVGMSPNPLIEYIVENFCTNVPSTGATLGECTSDGSVYDIYR 119
|||
DB 91 ITFECTENPSGNAYLAVGWTSTPLVEYITLEDYDYNPNSMTYKGTVTSDGSVYDIYE 150
|||
QY 120 TORVNPSTIGTATFYQYVSWYVRNHRSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 179
|||
DB 151 HQQVNPSTISGATATFNQWSTKQNTRSSGTVTANHFNAKGLGNLGSFNYQIVSTEGY 210
|||
QY 180 FSSGSASITVS 190
|||
DB 211 ESSGSSTITS 221
|||

RESULT 12

endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
S43919
C/Species: Humicola insolens
C/Date: 19-Mar-1997 #revision 19-Mar-1997 #text_change 22-Jun-1999
C/Accession: S43919
R/Dalboge, H.; Heldt-Hansen, H.P.
Mol. Gen. Genet. 243, 253-260, 1994
A/Title: A novel method for efficient expression cloning of fungal enzyme genes.
A/Reference number: S43919; MUID:94247364; PMID:9190078
A/Accession: S43919
A/Molecule type: mRNA
A/Residues: 1-227 <DAL>
A/Cross-references: EMBL:X76047; NID:9505260; PIDN:CA53632.1; PID:9505261
C/Genetics:
A/Gene: xyl1
C/Function:
A/Pathway: xylan degradation
C/Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C/Keywords: glycosidase; hydrolase; polysaccharide degradation
F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
F.48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F.112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
F.121,212/Active site: Glu #status predicted

Query Match 58.4%; Score 617.5; DB 2; Length 227;
Best Local Similarity 58.8%; Pred. No. 3.9e-41;
Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

QY 8 GYNNGYFYSYWNNDHGQVYTYNPGQGFVSVMNSGNGFVGKGMQPTKXKV 67
|||
DB 44 GHHNNGFYFYSWMDHGQVYTYNPGQGFVSVMNSGNGFVGKGMQPTKXKV 102
|||
QY 68 PNGNSYLVYVWGRPLLEFYIVENFCTNVPSTGATLGECTSDGSVYDIYR 127
|||
DB 103 PQNGSLAVYVWGRPLLEFYIVENFCTNVPSTGATLGECTSDGSVYDIYR 162
|||
QY 128 IIGTATFYQYVSWYVRNHRSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 187
|||
DB 153 IDGTATFYQYVSWYVRNHRSSGSVNTANHFNCWAQHGLTLGTMDYQIVAVEGY 222
|||
QY 188 TV 189

DB 223 YV 224

RESULT 13

US0590
endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
N/Alternate names: xylanase B
C/Species: Streptomyces lividans
C/Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
C/Accession: US0590; P30239
R/Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
Gene 107, 75-82, 1991
A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
A/Reference number: US0589; MUID:92077439; PMID:1743521
A/Accession: US0590
A/Molecule type: DNA
A/Residues: 1-333 <SHA>
A/Cross-references: GB:M64552
A/Accession: P30239
A/Molecule type: protein
A/Residues: 41-71 <SH2>
C/Genetics:
A/Gene: xlnB
C/Function:
A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
A/Pathway: xylan degradation
C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F.1-40/Domain: signal sequence #status predicted <SIG>
F.41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
F.54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
F.127,217/Active site: Glu #status predicted

Query Match 54.9%; Score 581; DB 1; Length 333;
Best Local Similarity 53.5%; Pred. No. 4.2e-38;
Matches 106; Conservative 33; Mismatches 43; Indels 16; Gaps 5;

QY 5 PGT-----GYNNGYFYSYWNNDHGQVYTYNPGQGFVSVMNSGNGFVGKGMQ 52
|||
DB 35 PGTADQVTVYTNQEGTNNNGYYSFWTDSQGTVMNMGSGQYSTWRNTGNVAAKGVA 94
|||
QY 53 PGTNKYINFSGYNPNNGSYLVYVGMSPNPLIEYIVENFCTNVPSTGATLGECTSDG 112
|||
DB 95 NGR-RIVQYSSGFNSGNAYLAVGWTSTPLVEYITLEDYDYNPNSMTYKGTVTSDG 151
|||
QY 113 SYVDIYRTORVNPSTIGTATFYQYVSWYVRNHRSSGSVNTANHFNCWAQHGLTLGTMD-Y 171
|||
DB 152 GTVDIYRTORVNPSTIGTATFYQYVSWYVRNHRSSGSVNTANHFNCWAQHGLTLGTMD-Y 211
|||
QY 172 QIVAVEGYFSSGSASITV 189
|||
DB 212 MIMATBGYSSTITS 229
|||

RESULT 14

US0601
endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
N/Alternate names: xylanase B
C/Species: Streptomyces coelicolor
C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C/Accession: US0601
R/Denabach, M.; Kleeer, H.M.; Denapalte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw
Mol. Microbiol. 21, 77-96, 1996
A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
A/Reference number: Z20556; MUID:97000351; PMID:8843436
A/Accession: US0601
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-335 <RED>
A/Cross-references: EMBL:AL133220; PIDN:CA61738.1
A/Experimental source: strain A3(2)
C/Genetics:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 14:25:54 ; Search time 14 Seconds

(without alignments)
706.666 Million cell updates/sec

Title: US-09-856-025B-63
Perfect score: 1058
Sequence: 1 QTIQPTGYNGYFYSYWN.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1031	97.4	222	1 XYN2_TRIRE	P36217 trichoderma
2	989	93.5	190	1 XYN1_TRLHA	P48793 trichoderma
3	674.5	63.8	225	1 XYN1_EMENT	P55332 emericella
4	666.5	63.0	225	1 XYNB_ASPKA	P48824 aspergillus
5	663.5	62.7	221	1 XYN2_EMENT	P55333 emericella
6	654.5	61.9	225	1 XYN2_ASPNG	P55330 aspergillus
7	639.5	60.4	221	1 XYN1_COCCA	Q05562 cochlidiobolus
8	625.5	59.1	225	1 XYN1_THELA	Q43097 thermomyces
9	617.5	58.4	227	1 XYNB_HUMIN	P55334 humicola
10	594	55.2	235	1 XYNB_STRLI	P26515 streptomyces
11	564.5	53.4	233	1 XYN2_MAGGR	P55335 magaporthe
12	564.5	53.4	644	1 XYN2_CELFI	P54865 cellulomonas
13	555.5	52.5	197	1 XYNB_SCHCO	P35809 schizophy11
14	517	48.9	240	1 XYN1_STRLI	P26220 streptomyces
15	514.5	48.6	210	1 XYNB_BACST	P45705 bacillus st
16	502	47.4	213	1 XYNB_BACST	P18429 bacillus st
17	501	47.4	213	1 XYNB_BACST	P08950 bacillus st
18	457	43.2	228	1 XYNB_BACST	P06964 bacillus pu
19	443.5	41.9	261	1 XYNB_CLOSA	P17137 clostridium
20	436	41.2	512	1 XYNB_CLOSA	P35558 clostridium
21	433	40.9	211	1 XYN1_ASPAV	P55328 aspergillus
22	433	40.9	211	1 XYN1_ASPNG	P55329 aspergillus
23	432.5	40.9	229	1 XYN1_TRIRE	P36218 trichoderma
24	431	40.7	211	1 XYN1_ASPPU	P55331 aspergillus
25	428	40.5	211	1 XYN3_ASPKA	P35557 aspergillus
26	392	37.1	954	1 XYNB_RUMFL	P21126 ruminococcu
27	377.5	35.7	802	1 XYNB_RUMFL	Q05317 ruminococcu
28	363.5	34.4	179	1 XYNB_PSEXY	P85123 pseudobuty
29	294	27.8	607	1 XYNB_NEOPA	P29127 neocallima
30	282.5	26.7	608	1 XYNB_FIBST	P36811 fibroclacter
31	242	22.9	625	1 XYNB_FIBST	Q16667 piromyces s
32	102	9.6	513	1 GUX1_TRIVI	P19355 trichoderma
33	98.5	9.3	159	1 GRPA_MEDFA	Q09134 medicago fa

RESULT 1	ALIGNMENTS
34 98 9.3 513 1 GUX1_TRIRE	P00725 trichoderma
35 97 9.2 454 1 PHA1_PSELE	P52000 pseudomonas
36 94 8.5 452 1 GUX1_CRYPA	Q00548 cryptosporid
37 92 8.7 734 1 PSAB_WHEAT	P58346 triticum ae
38 92 8.7 735 1 PSAB_MAIZE	P04967 zea mays (m
39 91 8.6 1829 1 FRPC_NEIMB	Q91905 neisseria m
40 90 8.5 358 1 RO22_XENLA	P15930 xenopus lae
41 90 8.5 734 1 PSAB_PINTH	P41640 pinus thunb
42 89.5 8.5 666 1 MUR2_ENTHR	P39046 enterococcu
43 89.5 8.5 708 1 QHED_COMTE	Q46444 comamonas t
44 89 8.4 341 1 ROA2_MOUSE	O88569 mus musculu
45 89 8.4 734 1 PSAB_PINKO	Q85wx0 pinus korai

RESULT 1	ALIGNMENTS
AC XYN2_TRIRE STANDARD; PRT; 222 AA.	
AC P36217;	
DT 01-JUN-1994 (Rel. 29, Created)	
DT 01-JUN-1994 (Rel. 29, Last sequence update)	
DT 28-FEB-2003 (Rel. 41, Last annotation update)	
DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)	
DE (1,4-beta-D-xylan xylanohydrolase 2).	
GN XYN2.	
OS Trichoderma reesei (Hypocrea jecorina).	
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.	
OX NCBI_TaxID=51453;	
RN [1]	
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.	
RP STRAIN=C30;	
RC MEDLINE=93103679; PubMed=1369024;	
RA Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,	
RA Harkki A., Kubicek C.P.;	
RT "The two major xylanases from Trichoderma reesei: characterization of	
RT both enzymes and genes.";	
RL Biotechnology 10:1461-1465 (1992).	
RN [2]	
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).	
RP STRAIN=C30;	
RC MEDLINE=94283373; PubMed=8013449;	
RA Toerrien A., Harkki A., Rouvinen J.;	
RT "Three-dimensional structure of endo-1,4-beta-xylanase II from	
RT Trichoderma reesei: two conformational states in the active site.";	
RL EMO J. 13:2493-2501 (1994).	
RN [3]	
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).	
RP STRAIN=C30;	
RC MEDLINE=95127663; PubMed=7827044;	
RA Toerrien A., Rouvinen J.;	
RT "Structural comparison of two major endo-1,4-xylanases from	
RT Trichoderma reesei.";	
RL Biochemistry 34:847-856 (1995).	
RN [4]	
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).	
RP STRAIN=C30;	
RC MEDLINE=96302263; PubMed=8755744;	
RA Havukainen R., Toerrien A., Laitinen T., Rouvinen J.;	
RT "Covalent binding of three epoxalyxl xylosides to the active site of	
RT endo-1,4-xylanase II from Trichoderma reesei.";	
RL Biochemistry 35:9617-9624 (1996).	
CC -1- CATALYTIC ACTIVITY: Endomycrolysis of 1,4-beta-D-xylosidic	
CC linkages in xylans.	
CC -1- PATHWAY: Xylan degradation.	
CC -1- PPM: The N-terminus is blocked.	
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl	
CC hydrolases).	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	

FT	STRAND	182	190
SQ	SEQUENCE	190 AA:	20703 MW; 6A0F4DC359C698 CRC64;
	Query Match	93.5%;	Score 989; DB 1; Length 190;
	Best Local Similarity	93.7%;	Pred. No. 8.5e-76;
	Matches 178; Conservative	4;	Mismatches 8; Indels 0; Gaps 0
Qy		1	OTIQGTGVNNNGYEFYSVYNNDGCGVTATNMGPGSGFSVMKNSGNVVGKGMPGPKNYI 60
Dd		1	QTIGGCTGVSNXYISIVYINMDHAGVTTITNGGGSTFVMSNSGNFVAGKGMPGPKNYI 60
Qy		61	NFGSGSYNNGNSYLSLVGMSRNPDI.EYIIVENFGTYPNSTGATKLGECTSDOSVVDIYRT 120
Dd		61	NFGSGSYNNGNSYLSLVGMSRNPDI.EYIIVENFGTYPNSTGATKLGECTSDOSVVDIYRT 120
Qy		121	QRVNPPSLTGNTFFQVMSYVRNRNHSSSGSVFNTANFNPCMAOGLTLGITMDIYVAVEGYF 180
Dd		121	QRVNPPSLTGNTFFQVMSYVRNRNHSSSGSVFNTANFNMAASHGLTLGITMDIYVAVEGYF 180
Qy		181	SSGSASITVS 190
Dd		181	SSGSASITVS 190
		190	SSGSASITVS 190
		190	SSGSASITVS 190
RESULT 3			
XNYI	EMENTI		
ID	_XNYI	EMENTI	STANDARD; PRT; 225 AA.
AC	P55332;	C00173;	
DT	01-OCT-1996	(Rel. 34,	Created)
DT	01-OCT-1996	(Rel. 34,	Last sequence update)
DT	28-FEB-2003	(Rel. 41,	Last annotation update)
D3	Endo-1,4-beta-xylanase 1 precursor (BC 3.2.1.8) (Xylanase 1)		
D3	De (1,4-beta-D-xylan xylanohydrolase 1).		
CS	Emericella nidulans (Aspergillus nidulans).		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
CC	Eurotiales; Trichocomaceae; Emericella.		
OX	NCBI_TaxID=162425;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96236210; PubMed=8787417;		
RA	Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;		
RT	"Molecular cloning and expression in Saccharomyces cerevisiae of two		
RT	Aspergillus nidulans xylanase genes";		
RL	Appl. Environ. Microbiol. 62:2179-2182 (1996).		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic		
CC	linkages in xyans.		
CC	-1- PATHWAY: Xylan degradation.		
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl		
CC	hydrolases).		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (see http://www.isb-sdb.ch/announce/		
CC	or send an email to license@isb-sdb.ch).		
CC	-----		
DR	EMBL; Z49892; CAAG0073.1; .		
DR	PIR; S57477; S57477.		
DR	HSSP; P48793; IXND.		
DR	InterPro; IPR008985; ConA_lke_1ec_gf.		
DR	InterPro; IPR00137; Glyco_hydro_11.		
DR	pfam; PF00457; Glyco_hydro_11.1.		
DR	PRINTS; PR00911; GLHYDRLASEB1.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KW	Xylan degradation; Hydrolase; Glycosidase; Signal.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	19	
FT	ACT_SITE	121	ENDO-1,4-BETA-XYLANSASE 1.
FT	ACT_SITE	212	NUCLEOPHILE (BY SIMILARITY).
FT	ACT_SITE	212	PROTON DONOR (BY SIMILARITY).
QO	SEQUENCE	225 AA;	24070 MW; PROTON DONOR (BY SIMILARITY). 620F2C79602CFEC CRC64;

```

Query Match 119: 63.0%; Score 674.5; DB 1; Length 225;
Best Local Similarity 65.0%; Pred. No. 1.8e-49;
Matches 119; Conservative 25; Mismatches .38; Indels 1; Gaps 1

QY 7 TGNNGYEYSYVNDHGGVYTYTNGPQGFYSVMSNSGNFVGKGNQPTKKNKVINFGSGY 66
DB 43 TQWSNGYYYSFMTGGCGDVITYTNGAGGSGSYTQWSNVGNFVGKGNPQS-TRTINYGGSF 101
QY 67 NPNGSYSYVYGVWBRNPLIEYIYVENPFTYMPSTGATLGECTSDGSYVDIYRTQVNP 126
DB 102 NPSNGIYIAVGMQNPFLIEYIYVSGTYNPGSGGHRGVYSNGATYDYIYATRYNAP 161
QY 127 SIIGTATFYQYVSVRRNRHSSGSVNTANHFNCMAQHGLTLTGMDYQIYAVESYFSSGSAS 186
DB 162 SIEGTATPECWVSRSQSKRTGTYTANHFAMALGRLGLTHNYQIYATREYSGSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
XNBN ASPKA
ID _XNBN ASPKA STANDARD; PRT; 225 AA.
AC P48824.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.6) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B).
GN XNBN
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OC NCBI_Taxid:40384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4308;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL; D38070; BA07264.1; -.
DR HSSP; P36217; IXYO.
DR InterPro; IPR006895; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00611; GHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F12_1; 1.
DR KX xylan degradation; Hydrolyase; glycosidase; signal.
FT CHAIN 1 18
FT SIGNAL 18
FT ACT_SITE 19 225
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match 63.0%; Score 666.5; DB 1; Length 225;
Best Local Similarity 65.0%; Pred. No. 8.4e-49;
Matches 119; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

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QY 7 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 66
 DB 43 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 101
 QY 67 NPNNGSYLVSWGMSNPLIEYIVENFGTVNPSGTATLGECTSDGSVYDIYRTORVNOP 126
 DB 102 TPGNGYLVSWGMSNPLIEYIVENFGTVNPSGTATLGECTSDGSVYDIYRTORVNOP 161
 QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGLTLGTMQYQIVAVEGYSGSGAS 186
 DB 162 SIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGLTLGTMQYQIVAVEGYSGSGAS 221
 QY 187 ITVS 189
 DB 222 ITVS 224

RESULT 5
 ID XYN2_EMENT STANDARD; PRT; 221 AA.

AC P55333; Q00176; 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
 DE (1,4-beta-D-xylan xylanohydrolase II).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; Emericella.
 ON NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9636210; PubMed=8787417;
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
 RT Molecular cloning and expression in *Saccharomyces cerevisiae* of two
 RT *Aspergillus nidulans* xylanase genes.
 RL Appl. Environ. Microbiol. 62:2179-2182 (1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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 CC or send an email to license@isb-sib.ch).

CC EMBL; Z49893; CAA90074.1; -.
 DR PIR; S57469; S57469.
 DR HSSP; P48793; 1XND.
 DR InterPro; IPR008985; Cona_1like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 221
 FT ACT_SITE 117 117
 FT ACT_SITE 208 208
 FT ACT_SITE 221 221
 SQ SEQUENCE 221 AA; 23517 MW; 4266E5E80DD39475 CRC64;

Query Match 62.7%; Score 663.5; DB 1; Length 221;
 Best Local Similarity 65.2%; Pred. No. 1.5e-48;
 Matches 120; Conservative 25; Mismatches 38; Indels 1; Gaps 1;
 7 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 66

DB 39 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 97
 QY 67 NPNNGSYLVSWGMSNPLIEYIVENFGTVNPSGTATLGECTSDGSVYDIYRTORVNOP 126
 DB 98 TPGNGYLVSWGMSNPLIEYIVENFGTVNPSGTATLGECTSDGSVYDIYRTORVNOP 157
 QY 127 SIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGLTLGTMQYQIVAVEGYSGSGAS 186
 DB 158 SIIGTATFYQYWSVRNRHSSGSVNTANHFNCMAQHGLTLGTMQYQIVAVEGYSGSGAS 217
 QY 187 ITVS 190
 DB 218 ITVS 221

RESULT 6
 ID XYN2_ASPNG STANDARD; PRT; 225 AA.

AC P55330; Q12557; 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
 DE (1,4-beta-D-xylan xylanohydrolase II).
 OS *Aspergillus niger*.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiiales; Trichocomaceae; *Aspergillus*.
 ON NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=IFO 4066;
 RA Ito K.;
 RT Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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CC EMBL; D18071; BAA07265.1; -.
 DR HSSP; P09850; 1XNB.
 DR InterPro; IPR008985; Cona_1like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 13
 FT PROPEP 19 37
 FT CHAIN 38 225
 FT ACT_SITE 121 121
 FT ACT_SITE 212 212
 SQ SEQUENCE 225 AA; 24057 MW; C4B8B007AB2B8FD CRC64;

Query Match 61.9%; Score 654.5; DB 1; Length 225;
 Best Local Similarity 64.5%; Pred. No. 8.4e-48;
 Matches 118; Conservative 22; Mismatches 42; Indels 1; Gaps 1;
 7 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 66
 DB 43 TGNNGYFYSYWMDGHCAGVYTTNGPGGQPSVNMNSGNFVGKGMQPGTKKXVINFSGSY 101

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QY 67 NENGNSYLSVGMGRNPLIEYVENFGTYPNPGATKLGECTSDGSVDYRTQVNOP 126
DB 102 TFSNGYLSVYGMTDPLEYIVSVSGYNNPGSGGTGYTSDGSVDYDITARTMAA 161
QY 127 SLIGATFTQYVSVRRNRHSSGSVNTANFNCAQCHGLTGLTMDYQIYAVESGSSGAS 186
DB 162 SLQGATFTQYVSVRRNRHSSGSVNTANFNCAQCHGLTGLTMDYQIYAVESGSSGAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 7
XVNL COCCA STANDARD; PRT; 221 AA.
AC 006562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase 1).
GN XV1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OX Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB111;
RC MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaccione D.G., Holden F.R., Walton J.D.;
RT "Cloning and targeted gene disruption of XV1, a beta 1,4-xylanase
RT gene from the maize pathogen Cochliobolus carbonum.";
RL Mol. Plant Microbe Interact. 6:467-473 (1993).
[2]
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RT "Xylanases from the fungal maize pathogen Cochliobolus carbonum.";
RL Physiol. Mol. Plant Pathol. 40:39-47 (1992).
CC -1- FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
CC EMBL, U13596; AAA33024.1; -.
CC HSSP; O43097; 1YNA.
DR InterPro; IPR008985; ConA like lec_g1.
DR InterPro; IPR001137; glyco_hydro_11.
DR Pfam; PF00457; glyco_hydro_11; 1.
DR PRINTS; PR00911; GHYDRASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 30
FT CHAIN 31 221
FT ACT_SITE 115 115
FT ACT_SITE 206 206
FT ACT_SITE 206 206
FT ACT_SITE 81 81
FT CONFLICT 81 81
W -> I (IN REF. 2).

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FT CONFLICT 107 107 G -> A (IN REF. 2).
FT CONFLICT 131 131 S -> W (IN REF. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59DDB9831FC5B08C CRC64;
Query Match 60.4%; Score 639.5; DB 1; Length 221;
Best Local Similarity 61.1%; Pred. No. 1.5e-46;
Matches 116; Conservative 25; Mismatches 48; Indels 1; Gaps 1;
QY 1 QTIQPTGYNNGSYLVYGMGRNPLIEYVENFGTYPNPGATKLGECTSDGSVDYRT 60
DB 31 QNTNNGEGTNGCGWMSDGCARATYTNAGGSYSVMSGGNLYGKGMNPGTA RTI 85
QY 61 NFGSYNPNNGNSYLSVYGMGRNPLIEYVENFGTYPNPGATKLGECTSDGSVDYRT 120
DB 90 TYSGTYNNGNSYLAAYGWMTRNPLVEYVENFGTYDPSQSQNKGTVTSDGSSYKLAQS 149
QY 121 QRVNPSIIGTATFTQYVSVRRNRHSSGSVNTANFNCAQCHGLTGLTMDYQIYAVESGF 180
DB 150 TRNQPSTIDGTRFTQYVSVRRNRHSSGSVNMKTHPDWASKGNLQGHYYQIYVATEGVF 209
QY 181 SSGSASITVS 190
DB 210 STGNAGITVN 219

RESULT 8
XVNA THELA STANDARD; PRT; 225 AA.
AC 043097;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
DE xylan xylanohydrolase).
GN XVNA.
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; Mitosporici Ascomycota; Thermomyces.
OX NCBI_TaxID=5541;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 5826 / Tsiklinsky;
RC MEDLINE=97033440; PubMed=8879171;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable
RT xylanase Xvna from Thermomyces lanuginosus.";
RL J. Biotechnol. 49:211-218 (1996).
[2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RC MEDLINE=98426042; PubMed=9753433;
RA Gruber K., Kintschar G., Hayn M., Schlacher A., Steiner W.,
RA Krecky C.;
RT "Thermophilic xylanase from Thermomyces lanuginosus: high-resolution
RT X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485 (1998).
CC -1- FUNCTION: THERMOSTABLE XYLANASE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC -----
CC EMBL, U15436; AB94633.1; -.
CC PDB; 1YNA; 12-FEB-97.
DR InterPro; IPR008985; ConA like lec_g1.

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DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;
 KM Pyrolicidone carboxylic acid.
 FT SIGNAL 1 31
 FT CHAIN 32 225
 FT ACT SITE 117 117 ENDO-1,4-BETA-XYLANASE.
 FT MOD RES 32 32 NUCLEOPHILE.
 FT MOD RES 32 32 PROTON DONOR.
 FT DISULFID 141 185 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 33 33
 FT STRAND 37 41
 FT STRAND 42 43
 FT STRAND 44 50
 FT STRAND 45 60
 FT STRAND 56 64
 FT STRAND 63 64
 FT STRAND 65 70
 FT STRAND 75 82
 FT STRAND 90 100
 FT STRAND 103 112
 FT STRAND 113 115
 FT STRAND 116 124
 FT STRAND 129 132
 FT STRAND 134 141
 FT STRAND 142 143
 FT STRAND 144 158
 FT STRAND 159 160
 FT STRAND 161 172
 FT STRAND 179 182
 FT HELIX 183 192
 FT TURN 193 194
 FT TURN 200 211
 FT STRAND 214 223
 SQ SEQUENCE 225 AA; 24355 MW; FAA79A914C5C676C CRC64;

Query Match 59.1%; Score 625.5; DB 1; Length 225;
 Best Local Similarity 59.2%; Pred. No. 2.2e-45;
 Matches 113; Conservative 28; Mismatches 49; Indels 1; Gaps 1;

DR 1 QTIQGTGNNKGFYSYNDGHSYTYNPGGQFSVNMNSGNFVGGKMGKMPGKXKVI 60
 DB 32 QTPNSEGHDGYYSWSDGGAQATYTNLEGGTYEISWGQGNLVGGKMPGLNAPAI 91
 QY 61 NFGSGYNPNNGSYLVYVGMRSNPLLEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120
 DB 92 HREGYVQNGNSYLAIVGWTNPLVEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 151
 QY 121 QGVNOPSITGATFYQVSVRRNHSNPGSVNTAHFNCAOHGLTL-GTMDYQIYAVBGY 179
 DB 152 TRVNAPSIDGTQTFQYWSVRODKRTSGTVOTGCHFDAMARAGLNVDHXYQIVATGEGY 211
 QY 180 FSSGSASITVS 190
 DB 212 FSSGYARITVA 222

RESULT 9
 XYNL_HUMIN STANDARD; PRT; 227 AA.
 ID XYNL_HUMIN STANDARD; PRT; 227 AA.
 AC P55334; Q12625; Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 DE (1,4-beta-D-xylan xylanohydrolase 1).
 GN XYL1
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 ON NCBI_TaxID=34413;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=9424764; PubMed=8190078;
 RA Dalbeige H., Hansen H.P.H.,
 RT "A novel method for efficient expression cloning of fungal enzyme
 gene.";
 RL Mol. Gen. Genet. 243:253-260(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 DR EMBL; X76047; CAA53632.1; -.
 DR PIR; S43919; S43919.
 DR HSP; O43097; 1YNA.
 DR InterPro; IPR006985; Cons like lec.g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 227
 FT ACT SITE 121 121 ENDO-1,4-BETA-XYLANASE 1.
 FT ACT SITE 212 212 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCEAD1F CRC64;

Query Match 58.4%; Score 617.5; DB 1; Length 227;
 Best Local Similarity 58.8%; Pred. No. 1e-44;
 Matches 107; Conservative 26; Mismatches 48; Indels 1; Gaps 1;

DR 8 GYNNGYFYSYNDGHSYTYNPGGQFSVNMNSGNFVGGKMGKMPGKXKVI 67
 DB 44 GYNNGYFYSYNDGHSYTYNPGGQFSVNMNSGNFVGGKMGKMPGKXKVI 102
 QY 68 PGNSTLSYVGMRSNPLLEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 127
 DB 103 PGNSTLSYVGMRSNPLLEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 162
 QY 128 IIGTATFYQVSVRRNHSNPGSVNTAHFNCAOHGLTLGTMDYQIYAVBGY 187
 DB 163 IIGTATFYQVSVRRNHSNPGSVNTAHFNCAOHGLTLGTMDYQIYAVBGY 222
 QY 188 TV 189
 DB 223 YV 224

RESULT 10
 XYNL_STRLI STANDARD; PRT; 335 AA.
 ID XYNL_STRLI STANDARD; PRT; 335 AA.
 AC P26515;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
 DE (1,4-beta-D-xylan xylanohydrolase B).
 GN XYNB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptomycetaceae; Streptomyces.
 ON NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.

```

RC STRAIN=66 / 1326; PubMed=1745321;
RX MEDLINE=92077439;
RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluempfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
RL lividans.";
RL Gene 107:75-82(1991).
RN [2]
RP REVISIONS TO 29-32 AND 252-307.
RX STRAIN=66 / 1326;
RX MEDLINE=95189090; PubMed=7533741;
RA Shareck F., Biely P., Morosoli R., Kluempfel D.;
RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
RL reveals genes encoding acetyl xylan esterase and the RNA component of
RT ribonuclease P.";
RL Gene 153:105-109(1995).
RN [3]
RP REVISION TO 225.
RA Shareck F.;
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
CC component of plant cell-walls. XlnA and XlnB seem to act
CC sequentially on the substrate to yield xylobiose and xylose
CC as carbon sources.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL; M64552; AAC06114.2; -.
DR HSBP; P09650; IXNB.
DR InterPro; IPR001919; Bac_cellose-bind.
DR InterPro; IPR008965; Cellul bind.
DR InterPro; IPR008985; Coma_like_deg_gl.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRASE11.
DR SMART; SM00637; CBD_11; 1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 41
FT CHAIN 42 335
FT DOMAIN 42 230
FT DOMAIN 231 249
FT DOMAIN 250 335
FT ACT_SITE 128 128
FT ACT_SITE 218 218
FT ACT_SITE 335 AA; 35575 MW; 518145888PROF C6G64;
SQ SEQUENCE 335 AA; 35575 MW; 518145888PROF C6G64;

```

Query Match	55.2%	Score	584	DB	1	Length	335
Best Local Similarity	54.0%	Pred.	No. 1e-41				
Matches	107	Conservative	32	Mismatches	43	Indels	16
						Gaps	5

QY 5 PGT-----GYNNGYFYYSWMDGHGGVITYLTPGQOFYSVNMNSQNFVFGKMQ 52

Db 36 PGTAAADIVTTLTNOEGINNGYYSFWDISOGIVSMNMSSGGQYSTMTANTGTFVAGKKMA 95

QY 53 PGTAKVTVFSGSVNPNNSYLSVYGMSRNPITXYIENGTSPSGATKJGCTSDG 112

Db 96 NGR-RTQYSGSFPSGNATLALGWSNPLVEIYIYIDNMTYR-TGEYK-GVYIDG 152

QY 113 SVYDIYRTQYVNSPSTIGTATPQYWSVRNRHSSGVNTANHFNCMAQHGITGTMD-Y 171

D_b 153 GYTDIKTKTRVANKPSVEGRTFTDQYWSVRQSKRGCGITTTGNHDDAARARQMPJGNFSY 212

Q_y 172 QIVAVEGYFSSGSASTV 189
 |:| | | | | | | | |
D_b 213 MIMATEGYQSSGSSSINV 230

RESULT 11	
XYN2_MAGGR	
ID_XYN2_MAGGR	STANDARD;
	PRT: 233 AA.

AC P55335; 001171; Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Endo-1,4-beta-xylosylase 22 precursor (EC 3.2.1.8) (Xylanase 22)
DE (1,4-beta-D-xylosyl xylanoyldiolase 22).
DE XYN22.

RP SEQUENCE FROM N.A.
 RC STRAIN=KEN60-19;
 RX MEDLINE=96172742; PubMed=8589407;
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.,
 RT "Purification, cloning and characterization of two xylanases from
 RT Magnaporthe grisea, the rice blast fungus".
 EL Mol. Plant Microbe Interact. 8:506-514(1995).

CC
CC -1- CANNING ACTIVITY: Endonucleolytic cleavage of 1,4-beta-D-xylotetraose linkages in xylans.
CC
CC -1- PATHWAY: Xylan degradation.
CC
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl hydrolases).
CC
CC
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CC
CC

DR EMBL; U37529; AAC41683.1; -.
DR HSSP; O43097; 1YNA.
DR InterPro; IPR008985; ConA like lec st.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 39 POTENTIAL.
FT CHAIN 40 233 ENDO-1,4-BETA-XYLANASE 22.
FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CEC64;

Query Match	53.4%;	Score 564.5;	DB 1;	Length 233;
Best Local Similarity	51.3%;	Pred. No. 2.8e-40;		
Matches	98;	Conservative	34;	Mismatches 56; Indels 3; Gaps 2

QY	1	QRTPEGTGNNGGFFSYNNDHGVTYTNNGGGQFSTYMSNSGNFVGGCKGKQGETKAKVI	60
		
Db	40	QSTPSSTGHHNNYYYSMTDASPPQXONGNGGSSVQWMSGGAFVGGKMMGG-GRKSI	98
		
QY	61	NFGSGSYNP--NGNSLASYGMSRPNDLLEYLYVEVNFSGYTNSTGATKAGECTSDGSYVDI	118
		
Db	99	TYSGTFNPYNNNNALCLCYGWTQNDPLVEYLLYLVYSGYTNNGMSAQSGTGLAAGGTYTLH	158
		
QY	119	KTORVNVQBSIIETATFFQYTSYVRNRHNSGGSVANTAHFNCMAQGLTLGIMDYQIYAVBG	178
		
	159	ESIRVNVQPIBQTRFFQYQWALRQQRKNSGTVNNGEFPAMERKGMGNMHNHYIATG	218
		

CY	179	YFSSGSASITV	189
Dd	219	YRSGNSNINV	229
 RESULT 12 -----			
ID	_XYND_CELFI	STANDARD:	PRT; 644 AA.
AC	P54865;		
DT	01-OCT-1996	(Rel. 34, Created)	
DT	01-OCT-1996	(Rel. 34, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).		
GN	XYND.		
OS	Cellulomonas fimi.		
OC	Bacteria: Actinobacteriae; Actinobacteridae; Actinomycetales;		
OC	Micrococciaceae; Cellulomonadaceae; Cellulomonas.		
OX	NCB1_TextID=1708;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=221;		
RX	MEDLINE=94224155; PubMed=8170399;		
RA	Millward-Sadler S.J., Poole D.M., Henriessat B., Hazlewood G.P.,		
RA	Clarke J.H., Gilbert H.J.;		
RT	"Evidence for a general role for high-affinity non-catalytic		
RL	cellulose binding domains in microbial plant cell wall hydrolases.";		
RL	Mol. Microbiol. 11:375-382(1994).		
CC	-1- FUNCTION: Endo-acting xylanase which displays no detectable		
CC	activity against polysaccharides other than xylan. Hydrolyzes		
CC	glycosidic bonds with retention of anomeric configuration.		
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic		
CC	linkages in xyans.		
CC	-1- PATHWAY: Xylan degradation.		
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl		
CC	hydrolases).		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X76729; CA54145.1; .		
DR	PIR; I40712; I40712.		
DR	PDB; 1B5B; 2S-MAY-01.		
DR	PDB; 1B5C; 2S-MAY-01.		
DR	PDB; 1HEH; 10-MAY-01.		
DR	PDB; 1HEJ; 10-MAY-01.		
DR	PDB; 1XBD; 21-JUL-99.		
DR	PDB; 2XBQ; 21-JUL-99.		
DR	InterPro: IPRO01919; Bac celose-bind.		
DR	InterPro: IPRO09965; Cellul bind.		
DR	InterPro: IPRO09985; ConA-like lec.gl.		
DR	InterPro: IPRO01137; Glyco_hydro_11.		
DR	InterPro: IPRO02509; Polysac_deacet.		
DR	Pfam; PF00553; CBM_2; 2.		
DR	Pfam; PF00457; Glyco_hydro_11; 1.		
DR	Pfam; PF01522; Polysac_deacet; 1.		
DR	PRINTS; PR00911; GLHYDRLASE11.		
DR	SMART; SM00637; CBD_11; 2.		
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.		
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.		
KW	Xylan degradation; Hydrolase; Glycosidase; Signal; Repeat;		
KW	3D-structure.		
FT	SIGNAL	1	43 POTENTIAL.
FT	CHAIN	44	ENDO-1,4-BETA-XYLANASE D.
FT	DOMAIN	44	230 CATALYTIC.
FT	DOMAIN	231	LINKER ("HINGE") (GIV-RICH BOX).
FT	DOMAIN	246	2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.
FT	REPEAT	246	333

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FT REPEAT 557 644 2. LINKER ("HINGE") (PRO-THR BOX).
FT DOMAIN 337 350 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 548 556 POLY-GLY.
FT DOMAIN 231 238 POLY-GLY.
FT DOMAIN 241 245 POLY-GLY.
FT DOMAIN 548 558 POLY-GLY.
FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 644 AA; 66581 MW; 568045CE50E1820 CRC64;

Query Match 53.4%; Score 564.5; DB 1; Length 644;
Best Local Similarity 54.6%; Pred. No. 8.9e-40;
Matches 101; Conservative 38; Mismatches 41; Indels 5; Gaps 4

Db 49 TGNHDPYFSFWMDSGSVSMNLNSGGYT-RMSVITGFVAGKMSYGR-KTVSYSGQF 1066
7 TGNANFYFSYNWDGHGVTYTNNGQGFPSVWMSNSGPFVGKMGWQPTKXKTVNFSGSY 66
QY :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 49 TGNHDPYFSFWMDSGSVSMNLNSGGYT-RMSVITGFVAGKMSYGR-KTVSYSGQF 1066
QY 67 NPNGNSTLSYVGSKRPLLEYITVENPFTNPSTGATLTGECTSDGSVYDIYRQRYNP 126
Db 107 NPNRNAYLTLXGTOSSPLVEYIYVDSWGYRPT-GTFMGVTSDDGTYDTRQYVNAK 1644
QY 127 SIIG-FATPFQYWSVYRNHRSGSVNTANHFNCWQHGLTLGTMDYOIVAVEGYSSGSA 1853
Db 165 SIIGDSSTGYQVWSVYRQCKRTGTTISGHHDPDAAKSKMNLGRNNYIMMTEGYQSSGSS 2244
QY 186 SITVS 190
Db 225 SITVS 229

RESULT 13
XVNA SCHCO STANDARD; PRT; 197 AA.
ID XVNA SCHCO
AC P35809;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DB Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
DS XVNA.
GN Schizophyllum commune (Bracket fungus).
OS Eukaryote; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
CX NCBI_TaxId=5334;
XX
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 38548 / Delmar;
RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
RL (In) Visser J., Beldman G., Kusters-van Sommeren M.A.,
RL Voragen A.G.J. (eds.);
RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
RN [2]
RP SEQUENCE, AND DISULFIDE BONDS.
RC STRAIN=ATCC 38548 / Delmar;
RA MEDLINE=94063044; PubMed=823636;
RX Oka T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
RA Jurasek L., Palce M.G.;
RT "Amino acid sequence and thermostability of xylanase A from
RT Schizophyllum commune";
RL FEBS Lett. 334:296-300 (1993).
RN [3]
RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
RC STRAIN=ATCC 38548 / Delmar;
RA MEDLINE=94155888; PubMed=7906649;
RX Bray M.R., Clarke A.J.;
RT "Identification of a glutamate residue at the active site of xylanase
RT A from Schizophyllum commune";
RL Eur. J. Biochem. 219:821-827 (1994).
CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
CC xylanase has a very broad pH activity.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.

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CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC PIR: A44597; A44597.
CC HSSP: 043097; 1XNA.
CC InterPro: IPR008985; Consilike_1ec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase.
CC ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
CC FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
CC FT DISTLFD 111 160
CC SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FBE9 CRC64;

Query Match: 52.5%; Score 555.5; DB 1; Length 197;
Best Local Similarity 53.9%; Pred. No. 1,3e-397;
Matches 103; Conservative 34; Mismatches 47; Indels 7; Gaps 3;

QY 7 TGYNNGYYSYWNNDHGAVTYTNGGQFQSVNWS-NSGNFYGKGMQDPTKKNYINFGS 65
DB 7 TGTGGYYYSWMTDAGDQATYQNNNGGSYTLTWSGNNGLVGGKGMNGAASRSISYSGT 66
QY 66 YNPNGNSYLSYVGSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYDITQRYNQ 125
DB 67 YQPNNSYLSYVGSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYDITQRYNQ 126
QY 126 PSIIETATFYQYWSYVRNRHS-----SGSVNTANFNCAQGLTLGT-NDYQIYAAVEGY 179
DB 127 PSIDGTQTFEQPWSYVRNPKKAPGSSISGTVDQCHFDAMKGLGNLGSSEHNYQIYATG 186
QY 180 FSSGSASITVS 190
DB 187 QSSGTATITVT 197

RESULT 14
XNNA_STRLI STANDARD: PRT; 240 AA.
AC P26220;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
DE (1,4-beta-D-xylan xylanohydrolase C).
GN XINC.
OS Streptomyces lividans.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
RC STRAIN=66 / 1326;
RX MEDLINE=92077439; PubMed=1743521;
RA Shaeck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RA "Sequences of three genes specifying xylanases in Streptomyces
RT lividans."
RL Gene 107:75-82(1991).
CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
CC component of plant cell walls.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M6453; AA26836.1; -
CC EMBL: A25307; CA01768.1; -
CC PIR: J50591; J50591.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR008985; Consilike_1ec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC TIGRPMs: TIGR01409; TAT_signal_seg_1.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; Signal.
CC ACT_SITE 1 49
CC FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
CC FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match: 48.9%; Score 517; DB 1; Length 240;
Best Local Similarity 52.1%; Pred. No. 2,7e-36;
Matches 100; Conservative 30; Mismatches 52; Indels 10; Gaps 6;

QY 2 TIDPGTYNNNGYYSYWNNDHGAVTYTNGGQFQSVNWSNSGNFYGKGMQDPTKKNYIN 61
DB .55 TNGQGT---DGMYYSPFTDGGGSVMTLNGGGSYSTQWNTGNGFVAGKGMSTDDGN--VR 109
QY 62 FSGSYNENGSYLSYVGSRNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYDITQRY 121
DB 110 YNGTFPVNGYGLIYMTNPLEYIYVENFGTNPSTGATKLGECTSDGSVDYDITQRY 167
QY 122 RVNQPSTIGTATFYQYWSYVRNRHS--VNTANFNCAQGLTLGTMD-YQIYAAVEG 178
DB 168 RYNAPSVGKTFTQYWSYVRQSVKTSSTGTTTGNHFDAMARAGMNGQFRYYIMATGEG 227
QY 179 YFSSGSASITVS 190
DB 228 YQSSGSSEITVS 239

RESULT 15
XNNA_BACST STANDARD: PRT; 210 AA.
ID P45705;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
DE (1,4-beta-D-xylan xylanohydrolase A).
GN XNNA.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=No. 236;
RA Cho S., Choi Y.;
RA "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
RT Bacillus stearothermophilus."
RL J. Microbiol. Biotechnol. 5:117-124(1995).
CC [2]
CC REVISIONS.
CC STRAIN=No. 236;
CC Cho S., Choi Y.;
CC Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.

```

CC -! SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U15985; AAB72117.1; -.
CC HSSP: P09850; 1XNB.
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 19
FT CHAIN 20 210 ENDO-1,4-BETA-XYLANASE A.
FT ACT_SITE 104 104 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 197 197 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 48.6%; Score 514.5; DB 1; Length 210;
Best Local Similarity 53.0%; Pred. No. 3,8e-36;
Matches 96; Conservative 30; Mismatches 46; Indels 7; Gaps 5;

QY 14 FYSYWNDEHGVTYTNRGQGFVYWNSSGNFVGKGMQPGTKNKVINP-SGSYNPNQNS 72
DB 31 YWQYWTDDGGWYNAVNGPGNYSVTWNTGNFVVGKWTGSPNRVINYNNAGIWEPSGNG 90
QY 73 YLSVYGMSENPILIEYIYVENFTYNPSTGATKLGECTSDGSVYDIYRQRYNQPSIICTA 132
DB 91 YLTLYGWTNNALIEYYVDSWGTYP-TGNYK-GTVNSDGGTYDYITTMRYNAPSIDQTQ 148
QY 133 TFEQYVSRYNRHRSRG--SVTANHFNCMAQHGLTG-TMDYQIVAVEGYFSSGSASIT 188
DB 149 TFGQFWSYRQSKRPFGSNVSIITFSNHYANAKSKMNLGSSWAIQVLAIEGYQSSGRSNVT 208
QY 189 V 189
DB 209 V 209

Search completed: August 17, 2004, 14:32:03
Job time : 15 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: August 17, 2004, 14:26:33 ; Search time 39 Seconds

(without alignments)
1537.140 Million cell updates/sec

Title: US-09-856-025B-63

Perfect score: 1 QTIQPGTGYNGYFYSYVND.....YQIVAEGRSSGSASITVS 190

Sequence: 1 QTIQPGTGYNGYFYSYVND.....YQIVAEGRSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

1017041

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP viirus:*
16: SP bacteriap:*
17: SP archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1031	97.4	223	3 Q02244	002244 trichoderma
2	1019	96.3	223	3 Q09015	099015 trichoderma
3	927	87.6	223	3 Q72803	072803 trichoderma
4	897	84.8	220	3 Q80074	081074 trichoderma
5	866	81.9	223	3 Q9JVF9	09JVF9 trichoderma
6	755.5	71.4	241	3 Q12580	012580 chaetomium
7	747.5	70.7	293	3 Q871E8	0871E8 neurospora
8	711.5	67.2	261	3 Q8J1V6	08J1V6 chaetomium
9	696.5	65.8	219	3 Q12579	012579 chaetomium
10	693.5	65.7	232	3 Q9HFA4	09HFA4 aspergillus
11	689.5	65.2	290	3 Q9H20	09H20 phanerochaete
12	689.5	65.2	290	3 Q9H20	09H20 phanerochaete
13	676.5	63.9	295	3 Q9CIR2	09CIR2 fusarium ox
14	669.5	63.3	227	3 Q00263	000263 ascocyta p
15	667.5	63.1	227	3 Q9UVZ3	09UVZ3 setosphaeri
16	655.5	62.0	225	3 Q8TG22	08TG22 aspergillus

17	649.5	61.4	230	3 Q8J1V5	08J1V5 chaetomium
18	646	61.1	221	3 Q9UV02	09UV02 penicillium
19	637.5	60.3	223	3 Q9H20	09H20 penicillium
20	633.5	59.9	231	3 Q13447	013447 cochlidiobol
21	631.5	59.7	283	3 Q96UV7	096UV7 lentimula e
22	631.5	59.7	346	2 Q8VUT4	08VUT4 pseudomonas
23	626.5	59.2	231	3 Q00350	000350 cochlidiobol
24	619.5	58.6	221	3 P87037	P87037 aspergillus
25	618.5	58.5	227	3 Q9HGE1	09HGE1 humicola gr
26	613.5	58.0	194	3 P81536	P81536 paecilomyce
27	608.5	57.5	335	2 Q08346	008346 streptomyce
28	608.5	57.5	335	2 Q9RMA4	09RMA4 streptomyce
29	607.5	57.4	335	2 Q9RQ38	09RQ38 promicromon
30	606.5	57.3	231	3 Q72A57	Q72A57 gibberella
31	606.5	57.3	338	2 Q56265	Q56265 thermomonos
32	596.5	56.4	221	3 Q9CIR1	09CIR1 fusarium ox
33	592	56.0	228	2 Q59962	Q59962 streptomyce
34	586.5	55.4	344	2 Q8GMV7	Q8GMV7 nonomuraea
35	585	55.4	216	3 Q74716	Q74716 claviceps p
36	583.5	55.2	329	2 Q9RWH9	Q9RWH9 streptomyce
37	581	54.9	335	16 Q9RKN6	Q9RKN6 streptomyce
38	561	53.0	191	2 Q9EW89	Q9EW89 streptomyce
39	533.5	50.4	661	2 Q59674	Q59674 pseudomonas
40	529	50.0	352	2 Q84DD2	Q84DD2 uncultured
41	523.5	49.5	666	2 Q59300	Q59300 cellvibrio
42	520.5	49.2	241	16 Q9R172	Q9R172 streptomyce
43	517.5	48.9	361	2 Q52375	Q52375 caldicellul
44	517	48.9	357	2 Q8VP72	Q8VP72 cellvibrio
45	515	48.7	240	2 Q56013	Q56013 streptomyce

ALIGNMENTS

RESULT 1
ID Q02244 PRELIMINARY; PRT; 223 AA.
AC Q02244;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endoxylanase II (EC 3.2.1.8) (Endo-L,4-beta-xylosidase).
GN X1N2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
KM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9408442; PubMed=8264524;
RA Saarelahti R., Paloheimo M., Fagerstrom R., Suominen P.L.,
RA Nevalainen K.M.;
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei
RT endoxylanase II (p1.9) gene xln2";
RL Mol. Gen. Genet. 241:497-503(1993).
CC -!- CATALYTIC ACTIVITY: ENDOLYXANOLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -!- PATHWAY: XYLAN DEGRADATION.
CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
EMBL: S673877, AAB29346.1, -.
CC PIR: S39883, S39883.
DR HSBP; P36217, IXYO.
DR GO: GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; Cons. like lec g1.
DR InterPro: IPR001137; Glyco hydro.11.
DR Pfam: PF00457; Glyco hydro.11.
DR PRINTS: PR00911; GHYDRLASE1.
DR PROSITE: PS00776; GLYCOSYL-HYDROL-F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL-HYDROL-F11_2; 1.
DR Glycosylase; Hydrolase; Xylan degradation.
KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22P9 CRC64;
SQ

Query Match 97.4%; Score 1031; DB 3; Length 223;
Best Local Similarity 98.4%; Pred. No. 3.2e-71;
Matches 187; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGPGGQSVNMSNGNFVGGKMGQPGTKNKVI 60
DB 34 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGPGGQSVNMSNGNFVGGKMGQPGTKNKVI 93
QY 61 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120
DB 94 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153
QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 180
DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

AC Q99015; 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreales; Hypocrea.
ON NCB1_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=QM 6a;
RA MEDLINE=97076932; PubMed=8975597;
RA la Grange D.C., Preforius I.S., van Zyl W.H.;
RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
RT Saccharomyces cerevisiae".
RL Appl. Environ. Microbiol. 62:1036-1044(1996).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DB EMBL; U24191; AB50278.1; -.
DB HSBP; P36217; IXYO.
DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; Cons. like lec 91.
DR InterPro; IPR001337; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Glycosidase; Hydrolase; Signal; Xylan degradation.
FT SIGNAL. 1
FT CHAIN 33
FT SEQUENCE 223 AA; 23981 MW; F696B545DAC30EB4 CRC64;

Query Match 96.3%; Score 1019; DB 3; Length 223;
Best Local Similarity 97.4%; Pred. No. 2.7e-70;
Matches 185; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGPGGQSVNMSNGNFVGGKMGQPGTKNKVI 60
DB 34 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGPGGQSVNMSNGNFVGGKMGQPGTKNKVI 93
QY 61 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120

DB 94 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153
QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 180
DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 3

Q72803 PRELIMINARY; PRT; 223 AA.

AC Q72803; 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
OS Trichoderma viride.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
ON NCB1_TaxID=5547;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XYUCC0183;
RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.J.,
RA Yang Z.W.,
RT Cloning and characterization of endo-1,4-beta-xylanase from
RT Trichoderma viride YUCC0183.
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY320048; AAP83925.1; -.
KW Glycosidase; Hydrolase; Xylan degradation.
SQ SEQUENCE 223 AA; 24218 MW; F3AF4E376FA03CAE CRC64;

Query Match 87.6%; Score 927; DB 3; Length 223;
Best Local Similarity 86.3%; Pred. No. 2.8e-63;
Matches 164; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGPGGQSVNMSNGNFVGGKMGQPGTKNKVI 60
DB 34 QTIQPGTGNNGYFVSYNNDGAGVTYTNNGAGGSVNMANGNFVGGKMGQPGTKNKVI 93
QY 61 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 120
DB 94 NFGSGYNPNNGSYLSVYGMSRNPLIEYIVENFGTYNPGTGATKLGECTSDGSVYDIYRT 153
QY 121 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 180
DB 154 QRYNQPSTIICTATFYQYWSVRNRHSSGGSVNTANHFNCMAQGLTLGTMVQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.

AC Q8J0T4; 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Xylanase.
OS Trichoderma sp. SY.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
ON NCB1_TaxID=215577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SY;
RA Min S.Y., Kim B.G., Ahn J.-H.;
RT "Purification, Characterization, and cDNA cloning of xylanase from

QY	Query Match	84.8%	Score 897	DB 3	Length 220
Db	Best local Similarity	83.7%	Pred. No. 5,4e-61		
	Matches 159	Conservative 11	Mismatches 20	Indels 0	Gaps 0
QY	1 QVICGCTGNNNGYEFYSYNNDDGGVGTNTNPGCGPSYNNKSGNFGVGGKMGCPGKHKMYI				
Db	31 QVICGCTGNNNGYEFYSYNNDDGGVGTNTNPGCGPSYNNKSGNFGVGGKMGCPGKHKMYI				
QY	61 NFGSGSYNNNGNSYLSVYGMRSNPLIEYIIVENFGTYNPGSTGATKLGECTSDGSVYDIYRT				
Db	91 NFGSGSYNNNGNSYLSVYGMRSNPLIEYIIVENFGTYNPGSTGATKLGECTSDGSVYDIYRT				
QY	121 QRVNPGSLITGRTFFQYMSVSRNHNHSSGSSYNTANFNFCNAGHGLLTGMDVQIVAVEGYF				
Db	151 QRVNPGSLITGRTFFQYMSVSRNHNHSSGSSYNTANFNFCNAGHGLLTGMDVQIVAVEGYF				
QY	181 SSGSASITVS 190				
Db	211 SSGSASITVS 220				
RESULT 5					
QY	Q9UVF9 PRELIMINARY; PRT; 223 AA.				
AC	Q9UVF9;				
DT	01-MAY-2000 (Tremblrel. 13, Created)				
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)				
DT	01-OCT-2003 (Tremblrel. 25, Last annotation update)				
DE	Emo-1,4-beta-xylanase precursor (EC 3.2.1.6).				
OS	Trichoderma virgide.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocressaceae; Hypocressales; mitosporic Hypocressales; Trichoderma.				
OX	NCBI_Taxid=5547;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Furman-Matarese N., Cohen E., Avni A.;				
RT	"Mutations in the Active Site of the Ethylene Inducing Xylanase				
RT	Elicitor Inhibits the D-1,4-Endoxylanase Activity But Not the				
RT	Elicitation Activity.";				
RL	Submitted (NCV-1998) to the EMBL/Genbank/DBJ databases.				
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLIDIC				
CC	LINKAGES IN XYLANS.				
CC	-1- PATHWAY: XYLAN DEGRADATION.				
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL				
CC	HYDROLASES).				
DR	EMBL; AJ012718; CAB60757.1; .				
DR	HSSP; P48793; 1XND.				
DR	GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR008985; Cona_like_deg_1.				
DR	Pfam; PF00457; Glyco_hydro_11; 1.				
DR	PRINTS; PR00911; GLHYDRASE11.				
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.				
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.				
DR	GLYCOSIDASE; Hydrolase; signal; xylan degradation.				
FT	SIGNAL 1 33 POTENTIAL.				
FT	CHAIN 34 223 ENDO-1,4-BETA-XYLANASE.				
SQ	SEQUENCE 223 AA; 24230 MW; F8B812028FB1212A CRC64;				

[illegible]

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL; D49850; BA08649.1; -

DR PIR; S71472; S71472.

DR HSP; P36217; 1X10.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR008985; Cons like lec.g1.

DR InterPro; IPR001137; Glyco_hydro.11.

DR Pfam; PF00457; Glyco_hydro.11; 1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.

KW Glycosidase; Hydrolyase; Xylan degradation.

SEQUENCE 219 AA; 23324 MW; 4729299808FD9BA CRC64;

Query Match 65.8%; Score 696.5; DB 3; Length 219;

Best Local Similarity 67.6%; Pred. No. 1.4e-45;

Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGNNNGYFYSYWNDHGQVITYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVNFSGS 65

DB 36 GTGNNNGYFYSPWTDGGDTVNYQNGAGGSYSVQWQNGFVGKGMNPGAA-RTINFGT 94

QY 66 VNPNGNSYLVYGMKSNPLIEYIVENFGTYNPSGATLGECTSDGSVDYIRYQRYNQ 125

DB 95 FSPQGGYLAIVGWTQNPVLEYIVESFGTYDSSQASKFTIQDGSSTYITAKTRVNO 154

QY 126 PSIIATFQYQWYVRNRHSSGSVNTAHFNCAQHGLTGTMDYQIVAAVEGYSSSGA 185

DB 155 PSIEGTSTDFQWVSQRNRRSSGSVVAHFANAGAKLGSHNYQIVATGYSOSSSS 214

QY 186 SITVS 190

DB 215 SITVS 219

RESULT 10

Q9HFA4 PRELIMINARY; PRT; 232 AA.

AC Q9HFA4; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XYN2.

OS Aspergillus oryzae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eucotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5062;

RN [1]

RP SEQUENCE FROM N.A.

RA Kimura T., Sakka K., Ohmura K.;

RT "Molecular cloning, overexpression, and purification of major xylanase from Aspergillus oryzae."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL; AB044941; BAB20794.1; -

DR PIR; JCT577; JCT577.

DR HSP; P36217; 1X10.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR008985; Cons like lec.g1.

DR InterPro; IPR001137; Glyco_hydro.11.

DR Pfam; PF00457; Glyco_hydro.11; 1.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.

KW Glycosidase; Hydrolyase; Xylan degradation.

SEQUENCE 232 AA; 24605 MW; 1f73104751EA561C CRC64;

Query Match 65.7%; Score 695.5; DB 3; Length 232;

Best Local Similarity 66.7%; Pred. No. 1.4e-45;

Matches 122; Conservative 26; Mismatches 34; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWNDHGQVITYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVNFSGS 66

DB 50 TGYNNGYFYSPWTDGGDVITYTNGGGSYSVQWQNGFVGKGMNPGS-SRATYSGSF 108

QY 67 NPNNSYLVYGMKSNPLIEYIVENFGTYNPSGATLGECTSDGSVDYIRYQRYNQ 126

DB 109 NPSNGYLAIVGWTQNPVLEYIVESGTYNPSGGSYKQVSDGTYNYIVSVRNAP 168

QY 127 SIITATFQYQWYVRNRHSSGSVNTAHFNCAQHGLTGTMDYQIVAAVEGYSSSGA 186

DB 169 SIITATFQWVSRTSKRVGTYTGNHNNAAKYLGLGTHNYQIVATGYSOSSGA 228

QY 187 ITV 189

DB 229 ITV 231

RESULT 11

Q9HEZ0 PRELIMINARY; PRT; 290 AA.

AC Q9HEZ0; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endo-1,4-B-Xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XYNB.

OS Phanerochaete chrysosporium.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Aphyllophorales; Corticiaceae; Phanerochaete.

OX NCBI_TaxID=5306;

RN [1]

RP SEQUENCE FROM N.A.

RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;

RT "Molecular characterization and expression analysis of two endo-1,4-B-Xylanase genes from Phanerochaete chrysosporium."

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

CC EMBL; AF301904; AG44994.1; -

DR HSP; P00725; 1A26.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR00254; CBD_fungal.

DR InterPro; IPR008985; Cons like lec.g1.

DR InterPro; IPR001137; Glyco_hydro.11.

DR Pfam; PF00734; CBM.1; 1.

DR Pfam; PF00457; Glyco_hydro.11; 1.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PRODOM; PD001821; CBD_fungal; 1.

DR SMART; SM00236; fCBD; 1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.

KW Glycosidase; Hydrolyase; Xylan degradation.

SEQUENCE 290 AA; 30425 MW; 6D1C6415370DA667D CRC64;

Query Match 65.2%; Score 689.5; DB 3; Length 290;

Best Local Similarity 64.2%; Pred. No. 5.2e-45;

Matches 122; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 1 OTTPGNGYNNGYFYSYWNDHGQVITYTNGPGQGFVSNMNSGNFVGKGMQPGTKNKNVI 60

DB 34 QSTPAGTNGNGYFYSPWTDGGSVTYNNGFAGEYSVTSMADNVAGKGMNPGSA-QAI 92

QY 61 NFGSGSYNNGNSYLSYVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSGVYDIYRT 120
 DB 93 SFTNAYQPNNGNSYLSYVGMNSTPLVEYIYLLDFGYNPAVSLTHKGLTISGATYDVYEG 152
 QY 121 QVNPQSIIGTATFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYF 180
 DB 153 TRVNPSPISGATFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYF 212
 QY 181 SSGSASTVTS 190
 DB 213 SSGSSTVTYN 222

RESULT 12

Q9HEV9 PRELIMINARY; PRT; 290 AA.

ID Q9HEV9
 AC Q9HEV9;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYNB.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCBI_Taxid=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K446;
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.,
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RT Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301905; AAG44995.1; -.
 DR HSSP; P00725; IAZ6.
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0004553; P:carbohydrate metabolism; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; ConA_like_1ec_g1.
 DR Pfam; PF00734; CBW_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fCBD_1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR GlycoBase; Hydrolyase; Xylan degradation.
 KW SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;
 SQ

Query Match 65.2%; Score 689.5; DB 3; Length 290;

Best Local Similarity 64.2%; Pred. No. 5.2e-45;

Matches 122; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 1 QTIOPGTGNGYFYSYNMDGAGVYTYNPGGQFVSVMNSNGNFGVGGKQMPGKXVY 60
 DB 34 QSTPAGTGTNGYFYSYNMDGAGVYTYNPGGQFVSVMNSNGNFGVGGKQMPGKXVY 92
 QY 61 NFGSGSYNNGNSYLSYVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSGVYDIYRT 120
 DB 93 SFTNAYQPNNGNSYLSYVGMNSTPLVEYIYLLDFGYNPAVSLTHKGLTISGATYDVYEG 152
 QY 121 QVNPQSIIGTATFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYF 180
 DB 153 TRVNPSPISGATFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYF 212
 QY 181 SSGSASTVTS 190
 DB 213 SSGSSTVTYN 222

Db 213 SSGSSTVTYN 222

RESULT 13

ID Q9CIR2 PRELIMINARY; PRT; 295 AA.

AC Q9CIR2;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Xylanase 5 protein (Ec 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYL5.
 OS Fusarium oxysporum f. sp. lycopersici.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 OX NCBI_Taxid=59765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hera C., Gomez-Gomez E., Ronceiro M.,
 RT "Cloning and characterization of two family 11 xylanase genes in
 RT Fusarium oxysporum f. sp. lycopersici."
 RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF246830; AAK27974.1; -.
 DR HSSP; O43097; IYNA.
 DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; ConA_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR GlycoBase; Hydrolyase; Xylan degradation.
 KW SEQUENCE 295 AA; 30858 MW; CA41056DCD3C104 CRC64;
 SQ

Query Match 63.9%; Score 676.5; DB 3; Length 295;

Best Local Similarity 64.1%; Pred. No. 5.2e-44;

Matches 118; Conservative 26; Mismatches 39; Indels 1; Gaps 1;

QY 7 TGNNGYFYSYNMDGAGVYTYNPGGQFVSVMNSNGNFGVGGKQMPGKXVY 66
 DB 40 SGTNNPFYSWMSDGGADATYTNGBEGGSYEMKQDGNVVGKQMSFG-KARTISYEY 98
 QY 67 NFGNSYLSYVGMNRNPLEYIVENFGTYNPGTATKLGECTSDGSGVYDIYRTQVNP 126
 DB 99 KPNNGSYLSYVGMNRNPLEYIVESFGTYNPGTATKLGCTVEADSTYDIFETRTNAP 158
 QY 127 SITGATFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYFSSGAS 186
 DB 159 SIDGTQFYQYVSVRNHRSSGSVNTANFNCAQHGTLTGMDYQIYAVEGYFSSGAS 218
 QY 187 ITVS 190
 DB 219 MTVS 222

RESULT 14

ID Q00263 PRELIMINARY; PRT; 227 AA.

AC Q00263;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-
 DE xylanase).
 GN Ascochyta pisi.
 OS Ascomycota; Pezizomycotina;
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 OC mitosporic Pezizomycotina; Ascochyta.

OX NCBI_TaxID=47971;
 RN [1]
 CC SEQUENCE FROM N.A.
 RA Lubbeck F.S., Paulin L., Degefu Y., Lubbeck M., Collinge D.,
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the
 RT phytopathogenic fungus *Ascochyta pisi* Lib.,"
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: Z68891; CAA93120.1; -.
 DR HSSP: O43097; IYNA.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; Consilike_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT SIGNAL 1
 FT CHAIN 19
 FT POTENTIAL.
 SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;
 Query Match 63.3%; Score 669.5; DB 3; Length 227;
 Best Local Similarity 64.2%; Pred. No. 1.3e-43;
 Matches 124; Conservative 21; Mismatches 43; Indels 5; Gaps 2;
 QY 2 TIQPGT---GYNNGYFYSYVNDGSGVYTYTNGPGGQFYSVWNSGNGFVGKGMOPGTKN 57
 Db 34 TARAGTPSSQGTGNGCFYSWMTDGAQATYTGAGGSSYVWVKTGNLVGGKMWPGAA- 92
 QY 58 KYINSGSYNPNGNSYLSYVWGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDI 117
 Db 93 RITTSYSGTSPGNSYLAIVGWTRNPLIEYIVENFGTYDPSQATVAGSSYKI 152
 QY 118 YRTQVNOPSIIIGTATFYQVSVRRNRRSSGSVNTANFNCAOHLTLGTMDYQIVAVE 177
 Db 153 AQGTQNPISIDGTQTFQYQVSVRRNRRSSGSVNMKTHFDAMAKGMKLGTHNQIVATE 212
 QY 178 GFSSGSASITVS 190
 Db 213 GFSSGSASITVN 225
 RESULT 15
 Q9UVZ3 PRELIMINARY; PRT; 227 AA.
 ID Q9UVZ3;
 AC Q9UVZ3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYL1
 OS Setosphaeria turcica.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
 OC Pleosporales; Pleosporaceae; Setosphaeria.
 OX NCBI_TaxID=93612;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H2;
 RA Degefu Y., Paulin L., Peraenen J., Lubbeck F.S.,
 RT "Cloning, sequencing and expression of a xylanase gene from the maize
 RT pathogen *Helminthosporium turcicum* Pass.,"
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DR EMBL: AJ238895; CAB52417.1; -.

DR HSSP: O43097; IYNA.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; Consilike_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT SIGNAL 1
 FT CHAIN 19
 FT POTENTIAL.
 SQ SEQUENCE 227 AA; 24123 MW; BA86FC075E5306E CRC64;
 Query Match 63.1%; Score 667.5; DB 3; Length 227;
 Best Local Similarity 63.7%; Pred. No. 1.3e-43;
 Matches 121; Conservative 22; Mismatches 46; Indels 1; Gaps 1;
 QY 1 QTIQPGTGYNNNGYFYSYVNDGSGVYTYTNGPGGQFYSVWNSGNGFVGKGMOPGTKN 60
 Db 37 QSTNGEGTNGGCTYSWMSDGAATTTNGAGSSYSVMGTGNTLVGGKMWPGTA-RTI 95
 QY 61 NFGSYNPNGNSYLSYVWGRNPLIEYIVENFGTYNPGTATKLGECTSDGSVYDI 120
 Db 96 TYSQYNPNGNSYLAIVGWTRNPLIEYIVENFGTYDPSQATVAGSSYKI 155
 QY 121 QRNVNPSIIIGTATFYQVSVRRNRRSSGSVNTANFNCAOHLTLGTMDYQIVAVE 180
 Db 156 TRNQPSIDGTQTFQYQVSVRRNRRSSGSVNMKTHFDAMAKGMKLGTHNQIVATE 215
 QY 181 SSGSASITVS 190
 Db 216 SSGSASITVN 225

Search completed: August 17, 2004, 14:32:55
 Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds
(without alignments)
1130.190 Million cell updates/sec

Title: US-09-856-025B-64
Perfect score: 1066
Sequence: 1 OTIOPGTGNNNGYFYSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneesep1960s:*
2: geneesep1960s:*
3: geneesep2000s:*
4: geneesep2000s:*
5: geneesep2002s:*
6: geneesep2003as:*
7: geneesep2003bs:*
8: geneesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	190	AAW60743	AAW60743 Xylanase
2	1017	95.4	190	AAW99680	AAW99680 T. reesei
3	1017	95.4	190	AAE18452	AAE18452 Trichoder
4	1017	95.4	190	AAO30259	AAO30259 Trichoder
5	1017	95.4	223	AAAR47122	AAAR47122 PI 9.0 en
6	1017	95.4	223	AAW67567	AAW67567 T. reesei
7	1015	95.2	190	AAW99735	AAW99735 Mutant T.
8	1014	95.1	190	AAE18470	AAE18470 Trichoder
9	1014	95.1	190	AAE18495	AAE18495 Trichoder
10	1014	95.1	190	AAO30300	AAO30300 Trichoder
11	1013	95.0	190	AAO30303	AAO30303 Trichoder
12	1013	95.0	190	AAO30301	AAO30301 Trichoder
13	1012	94.9	190	AAAB48541	AAAB48541 Trichoder
14	1012	94.9	190	AAO18647	AAO18647 T. reesei
15	1012	94.9	190	AAO30304	AAO30304 Trichoder
16	1011	94.8	190	AAO30299	AAO30299 Trichoder
17	1010	94.7	190	AAW68284	AAW68284 Modified
18	1010	94.7	190	AAE18471	AAE18471 Trichoder
19	1010	94.7	190	AAO30279	AAO30279 Trichoder
20	1009	94.7	190	AAE18496	AAE18496 Trichoder
21	1009	94.6	190	AAO30302	AAO30302 Trichoder
22	1008	94.6	190	AAO30280	AAO30280 Trichoder
23	1007	94.5	190	AAW60744	AAW60744 Xylanase
24	1007	94.5	190	AAW99681	AAW99681 T. vitide
25	1007	94.5	190	AAE18453	AAE18453 Trichoder

26	1006	94.4	190	AAO30306	AAO30306 Trichoder
27	1004	94.2	190	AAO30307	AAO30307 Trichoder
28	1001	93.9	190	AAO30305	AAO30305 Trichoder
29	1001	93.9	223	AAW57422	AAW57422 Amino aci
30	997	93.5	190	AAO30293	AAO30293 Trichoder
31	995	93.3	190	AAE18472	AAE18472 Trichoder
32	995	93.3	190	AAO30287	AAO30287 Trichoder
33	995	93.3	190	AAO30294	AAO30294 Trichoder
34	994	93.2	190	AAE48538	AAE48538 Trichoder
35	994	93.2	190	AAO18644	AAO18644 T. vitide
36	993	93.2	190	AAO30297	AAO30297 Trichoder
37	992	93.1	190	AAE18476	AAE18476 Trichoder
38	991	93.0	190	AAO30298	AAO30298 Trichoder
39	990	92.9	190	AAO30292	AAO30292 Trichoder
40	989	92.8	190	AAE18475	AAE18475 Trichoder
41	989	92.8	190	AAE18474	AAE18474 Trichoder
42	989	92.8	190	AAE18482	AAE18482 Trichoder
43	989	92.8	190	AAO30288	AAO30288 Trichoder
44	988	92.7	190	AAE18473	AAE18473 Trichoder
45	986	92.5	190	AAE18478	AAE18478 Trichoder

ALIGNMENTS

RESULT 1
AAW60743
ID AAW60743 standard; protein; 190 AA.
XX
AC AAW60743;
XX
DT 17-OCT-2003 (revised)
DT 02-SEP-1998 (first entry)
XX
DE Xylanase II of Trichoderma reesei.
XX
KW Family 11 xylanase; improve; thermophilicity; alkalophilicity;
KW thermostolerance; bleach; wood pulp; processing; wheat; maize;
KW digestibility-improving animal feed additive; starch production; mutant.
XX
OS Hypocrea jecorina.
XX
PN EP828002-A2.
XX
PD 11-MAR-1998.
XX
PF 05-SEP-1997; 97EP-00115412.
XX
PR 09-SEP-1996; 96US-00709912.
XX
PS (CANADA) NAT RES COUNCIL CANADA.
XX
PI Sung WL, Yaguchi M, Ishikawa K;
DR WPI; 1998-161100/15.
PT Modified xylanase enzymes - useful for improving wood pulp bleaching,
PT etc.
XX
PS Disclosure; Page 48; 84pp; English.
XX
CC AAW60728-44 represent family 11 xylanases. The specification describes a
CC method for modifying a family 11 xylanase to improve its thermophilicity,
CC alkalophilicity and/or thermostolerance. This method comprises
CC modification of amino acids 10, 27 or 29 of Trichoderma reesei xylanase
CC II or corresponding aligned amino acids of another family 11 xylanase,
CC replacement of one or more amino acid sequences in the N-terminal region
CC with corresponding aligned sequences from another family 11 xylanase to
CC form a chimeric xylanase and/or upstream extension of the N terminus by
CC addition of upto 10 amino acids. The modified xylanases are useful for
CC improving the bleachability of wood pulp by treatment at 55-75 degrees
CC Celsius and pH 7.5-9.0 for 5-180 minutes. They might also be useful as
CC digestibility-improving animal feed additives. They might also be useful

CC in the processing of wheat or maize for starch production. (Updated on 17
 CC -OCT-2003 to standardise OS field)
 XX
 SQ Sequence 190 AA;

Query Match 95.4%; Score 1017; DB 2; Length 190;
 Best Local Similarity 97.4%; Pred. No. 8e-86; 5; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGHHGVTYTNBPGGQFYSYVMSNSGNFVGGKMGQPGTKXKVI 60
 DB 1 QTIQPGTGYNNGYFYSYNDGHHGVTYTNBPGGQFYSYVMSNSGNFVGGKMGQPGTKXKVI 60
 QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSYDLYRT 120
 DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSYDLYRT 120
 QY 121 QRVNPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGMDYQIVAVEGYF 180
 DB 121 QRVNPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 2
 AA99680
 ID AA99680 standard; protein; 190 AA.

AC AAY99680;
 XX
 DT 12-SEP-2003 (revised)
 DT 28-SEP-2000 (first entry)
 XX
 DE T. reesei xylanase, Xyn II.

XX Xylanase; animal feed; digestion efficiency; thermostable;
 XX feed pelleting; enzyme; Xyn A; Xyn B; Xyn; Xyn C; Xyn I; Xyn II.
 XX Hypocrea jecorina.
 OS

PN WO200029587-A1.

XX 25-MAY-2000.

XX 16-NOV-1999; 99WO-CA001093.

XX 16-NOV-1998; 98US-0108504P.

XX (IOGE-) IOGEN CORP.

PI Sung WL, Tolan JS;

DR WPI; 2000-387799/33.

DR N-PSDB; AAA48219.

XX Thermostable xylanases useful for preparing animal feeds especially
 PT poultry or swine feed, exhibits optimal activity under physiological
 PT conditions.

PS Disclosure; Fig 1; 86pp; English.

XX Xylanase enzymes are added to animal feeds to increase the efficiency of
 CC digestion and assimilation of nutrients. Xylanases are preferentially
 CC added during the feed pelleting process. To survive the pelleting process
 CC and to have optimum activity in the animal, the xylanase needs to have
 CC high thermostability, with optimum activity at physiological pH and
 CC temperature. The present sequence, xylanase Xyn II, from *Trichoderma*
 CC reesei, is a xylanase family II member. The xylanases of family II have
 CC several properties suitable for feed applications, however, they lack the
 CC thermostability required to survive food pelleting. The present sequence
 CC was used to identify non-conserved residues in family II xylanases which

CC could be mutated to introduce desirable properties e.g. thermostability.
 CC As a result various thermostable xylanases were identified (AAY9683,
 CC AAY9684, AAY9685, AAY9686, AAY9725 and AAY9736) which would be
 CC useful for animal feeds, especially poultry and swine feed. (Updated on
 CC 12-SEP-2003 to standardise OS field)

XX Sequence 190 AA;

Query Match 95.4%; Score 1017; DB 3; Length 190;
 Best Local Similarity 97.4%; Pred. No. 8e-86; 5; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYNDGHHGVTYTNBPGGQFYSYVMSNSGNFVGGKMGQPGTKXKVI 60
 DB 1 QTIQPGTGYNNGYFYSYNDGHHGVTYTNBPGGQFYSYVMSNSGNFVGGKMGQPGTKXKVI 60
 QY 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSYDLYRT 120
 DB 61 NFSSSYNPNNGSYLSYVGMSSRNPLIEYIVENFGTNPSTGATKLGCVTSDGSYDLYRT 120
 QY 121 QRVNPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGMDYQIVAVEGYF 180
 DB 121 QRVNPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 3
 AA18452
 ID AA18452 standard; protein; 190 AA.

AC AA18452;

XX 29-AUG-2003 (revised)

DT 16-MAY-2002 (first entry)

XX Trichoderma reesei xylanase (Trx), Xyn II.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;
 XX pulp manufacture; poultry; swine feed; enzyme; Xyn II.

OS Hypocrea jecorina.

PH Key Location/Qualifiers

FT Region 151..162

XX /note="Helix"

PN WO200192487-A2.

XX 06-DEC-2001.

XX 31-MAY-2001; 2001WO-CA000769.

XX 31-MAY-2000; 2000US-0213803P.

XX (CANA) NAT RES COUNCIL CANADA.

PI Sung WL;

DR WPI; 2002-171435/22.

DR N-PSDB; AAD29410.

XX Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.

PS Disclosure; Page 80-81; 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also

CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx), Xyn II. (Updated on 29-AUG-2003 to standardise OS field)
 CC
 SQ Sequence 190 AA;

Query March 95.4%; Score 1017; DB 5; Length 190;
 Best Local Similarity 97.4%; Pred. No. 8e-86;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGFYFYSYNNNDHGCVTTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYNNGFYFYSYNNNDHGCVTTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLGTMDYQIVAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAHFNMAAQGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 4
 AA030259
 ID AA030259 standard; protein; 190 AA.

XX AA030259;
 AC
 XX 23-OCT-2003 (revised)
 DT 03-SEP-2003 (first entry)
 DE Trichoderma reesei xylanase II enzyme (Trx).
 XX
 KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KM pulp manufacture; poultry feed; swine feed; enzyme.
 XX
 OS Hypocrea jecorina.
 XX
 PN MO2003046169-A2.
 PD
 XX 05-JUN-2003.
 PE
 XX 20-NOV-2002; 2002MO-CA001758.
 FR 21-NOV-2001; 2001US-00990874.
 XX
 PA (CANADA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 XX
 DR WPI; 2003-513647/48.
 XX
 PT Novel modified xylanase useful in industrial process, exhibits improved
 PT thermostability, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.
 PS
 XX Claim 1; Fig 2; 105pp; English.
 CC The invention relates to modified xylanase enzyme which exhibits improved
 CC thermostability, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II enzyme. (Updated on 23-OCT-

CC 2003 to standardise OS field)

SQ Sequence 190 AA;

Query Match 95.4%; Score 1017; DB 7; Length 190;
 Best Local Similarity 97.4%; Pred. No. 8e-86;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGFYFYSYNNNDHGCVTTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYNNGFYFYSYNNNDHGCVTTNGPGQSFVSNMNSGNFVGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEIYIVENFGTNPSTGATKLGECTSDGSVYDIYRT 120
 QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLGTMDYQIVAVEGYF 180
 DB 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTAHFNMAAQGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 5
 AAR47122
 ID AAR47122 standard; protein; 223 AA.

XX AAR47122;
 AC
 XX 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 10-JUN-1994 (first entry)
 XX
 DE pi 9.0 endoxylanase.
 XX
 KW Trichoderma reesei; enzyme; paper; pulp; food; feed industry; pi 5.5;
 KM pi 9.0; xln1; xln2; endoxylanase.
 XX
 OS Hypocrea jecorina; QM6a.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 19..20
 FT Protein 34..223
 FT Modified-site 71
 FT /label= N-glycosylation_site
 FT Peptide 83..89
 FT /note= "sequence used for prepn. of PCR primer"
 FT Active-site 119
 FT /note= "Glu proposed to be involved with an active site"
 FT Active-site 210
 FT /note= "Glu proposed to be involved with an active site"
 XX
 PN MO9324621-A1.
 XX
 PD 09-DEC-1993.
 XX
 PF 24-MAY-1993; 93MO-FI000221.
 XX
 PR 29-MAY-1992; 92US-00868993.
 XX
 PA (ALKO-) ALKO CY AB.
 XX
 PI Suominen P, Nevalainen H, Saarelainen R, Paloheimo M, Lantinen T,
 PI Fagerstrom R;
 XX
 DR WPI; 1993-405812/50.
 DR N-PSDB; AA054775.
 XX

PT Isolated nucleic acid mol. used in enzymes for paper, pulp and feed
 PT industry - comprising sequence encoding amino acid sequence of T. reesei
 PT PI 5.5 xylanase.

PS Claim 3; Page 77-78; 11pp; English.

XX The T. reesei xln2 gene coding for the PI 9.0 endoxylanase was isolated
 CC from the wild-type strain QM6a. The gene contains one intron of 108
 CC nucleotides and codes for a protein of 223 amino acids in which two
 CC putative N-glycosylation target sites were found. Three different T.
 CC reesei strains were transformed by targeting a construct composed of the
 CC xln2 gene with its own promoter to the endogenous ch1 locus. Highest
 CC overall prodn. levels for xylanase were obtained using the T. reesei
 CC ALK02721, a genetically engineered strain, as a host. Integration into
 CC the ch1 locus was not required for enhanced expression under xln2
 CC promoter. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS
 CC field)

XX Sequence 223 AA;

Query Match 95.4%; Score 1017; DB 2; Length 223;
 Best Local Similarity 97.4%; Pred. No. 9.8e-86;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYWNDHGCVTYTNGPGQFSYVWMSNGNFVGGKMGQPGTKNKVI 60
 DB 34 QTIQPGTGNNGYFYSYWNDHGCVTYTNGPGQFSYVWMSNGNFVGGKMGQPGTKNKVI 93
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 153
 QY 121 QRVNOPSIIIGTATFYQYWSVRRNRHSSGSVNTACHFCNMAOHGLTLGTMQYQIVAVEGYF 180
 DB 154 QRVNOPSIIIGTATFYQYWSVRRNRHSSGSVNTAHNFNMAOQGLTLGTMQYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 6

AAM67567
 ID AAM67567 standard; protein; 223 AA.

XX AAM67567;

XX 17-OCT-2003 (revised)
 DT 02-MAR-1999 (first entry)

XX T. reesei xylanase II protein.

XX Xylanase; xln; reverse transcription; RT-PCR; primer; amplification;
 KW degradation; polymer; xylan; carbohydrate; plant; paper; pulp.

XX Hypocrea jecorina.

XX Key Location/Qualifiers

XX Peptide 1..19
 FT /note= "primary signal peptide"

XX Peptide 20..33
 FT /note= "propeptide"

XX Protein 33..223
 FT /note= "mature xylanase II protein"

XX Modified-site 71
 FT /note= "N-glycosylated"

XX Modified-site 94
 FT /note= "N-glycosylated"

XX Active-site 119
 FT /note= "active site residue"

XX Active-site 210
 FT /note= "active site residue"

XX US5637515-A.

XX 17-NOV-1998.

XX 16-SEP-1993; 93US-00121436.

XX 16-MAY-1990; 90US-00524308.

XX 29-MAY-1993; 92US-00869893.

XX 24-MAY-1993; 93MO-FI000221.

XX 18-JUN-1993; 93US-00078478.

XX (ALKO-) ALKO-YHTOET OY.

XX Palohelmo M, Nevalainen H, Saarelainen R, Fagerstrom R;

PI Suutinen P;

XX WPI; 1999-023453/02.

XX N-PSDB; AAVB1332.

XX Nucleic acids encoding Trichoderma reesei xylanase(s) - useful for

PT recombinant production of the enzyme, for use in paper and pulp

PT production.

PS Claim 3; Fig 3A-B; 52pp; English.

XX This sequence represents the Trichoderma reesei xylanase II enzyme (xln2)
 CC which has an isoelectric point (pI) of 9. The coding sequence was
 CC isolated by reverse transcription PCR using the primers AAVB1333-VB1335
 CC based on amino acid sequence derived from the N-terminal of the purified
 CC protein. The encoded protein contains a 33 amino acid propeptide sequence
 CC with a primary signal peptide cleavage site between residues 18-20. The
 CC mature protein comprises 190 amino acids with a calculated molecular
 CC weight of 20.8 kD. The enzymes are used in the degradation of the polymer
 CC xylan, one of the most abundant carbohydrate components in plants. This
 CC is especially useful in the paper and pulp making industry. (Updated on
 CC 17-OCT-2003 to standardise OS field)

XX Sequence 223 AA;

Query Match 95.4%; Score 1017; DB 2; Length 223;
 Best Local Similarity 97.4%; Pred. No. 9.8e-86;
 Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSYWNDHGCVTYTNGPGQFSYVWMSNGNFVGGKMGQPGTKNKVI 60
 DB 34 QTIQPGTGNNGYFYSYWNDHGCVTYTNGPGQFSYVWMSNGNFVGGKMGQPGTKNKVI 93
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYNPSGTATKLGECTCDGSVYDIYRT 153
 QY 121 QRVNOPSIIIGTATFYQYWSVRRNRHSSGSVNTACHFCNMAOHGLTLGTMQYQIVAVEGYF 180
 DB 154 QRVNOPSIIIGTATFYQYWSVRRNRHSSGSVNTAHNFNMAOQGLTLGTMQYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 7

AAV99735
 ID AAV99735 standard; protein; 190 AA.

XX AAV99735;

XX 12-SEP-2003 (revised)

DT 28-SEP-2000 (first entry)

XX Mutant T. reesei xylanase, Trx-162H.

XX Xylanase; animal feed; digestion efficiency; thermostable;

Query Match	95.2%	Score 1015;	DB 3;	Length 190;
Best Local Similarity	96.8%	Pred. No. 1,2e-85;		
Matches 184;	Conservative 1;	Mismatches 5;	Indels 0;	Gaps 0;
QY 1	CTIQPGCTVNNNGYFFSYNNNDHGCGTYYNNGPGCGQFSVNMNSNGNIVGKGKMQPGTKNKYI	60		
Db 1	CTIQPGCTVNNNGYFFSYNNNDHGCGTYYNNGPGCGQFSVNMNSNGNIVGKGKMQPGTKNKYI	60		
QY 61	NFSGSYNNENGNSYLSVYGMSENPLEIYYIVENFGTYNPNSTGATKLGECTCDGSVYDIYRT	120		
Db 61	NFSGSYNNENGNSYLSVYGMSENPLEIYYIVENFGTYNPNSTGATKLGECTCDGSVYDIYRT	120		
QY 121	QRVNOPSLITGATFYQYVSVRRNHRSSGSVNTACHFNCAOGLTLGTMDIQYIVAVEGYF	180		
Db 121	QRVNOPSLITGATFYQYVSVRRNHRSSGSVNTACHFNCAOGLTLGTMDIQYIVAVEGYF	180		
QY 161	SSGSASITVS 190			
Db 161	SSGSASITVS 190			

Key	Location/Qualifiers
Misc-difference 75	/note= "Wild type Ser substituted with Ala"
MO200192487-A2.	
06-DEC-2001.	
31-MAY-2001; 2001WO-CA000769.	
31-MAY-2000; 2000US-0213803P.	
(CANA) NAT RES COUNCIL CANADA.	
Sung WL;	
WPI; 2002-171435/22.	
Modified xylanase exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing.	
Claim 42; Page; 109pp; English.	
The present invention relates to a modified xylanase exhibiting increased thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase has improved performance at conditions of high temperature and pH and exhibits improved thermostability and/or alkalophilicity in comparison to corresponding native xylanase. The present sequence is Trichoderma reesei xylanase (Trx) mutant. Note: The present sequence is not shown in the specification but is derived from wild type xylanase referred as SEQ ID No: 16 (AAE18495) and shown in page 80-81 of the specification	
Sequence 190 AA;	
Query March	95.1%; Score 1014; DB 5; Length 190;
Best Local Similarity	96.8%; Pred. NO. 1.5e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;	
QY 1 QTIQPGTGYNGYFYSYMDGHGAVTYTNGPGQFQSVNMSNSGNFVGKGMQPGTKXKVI 60	
DB 1 QTIQPGTGYNGYFYSYMDGHGAVTYTNGPGQFQSVNMSNSGNFVGKGMQPGTKXKVI 60	
QY 61 NFGSGYNPNNSLSTLYGMRNPLIEYIYVENGTNPSTGAKRLGECICDGSVYIYR 120	
DB 61 NFGSGYNPNNSLSTLYGMRNPLIEYIYVENGTNPSTGAKRLGECICDGSVYIYR 120	
QY 121 QRNVQPSIIITAFYQWVSVRNHRSSGSVNTACFNCWAQHGLTGTMDYQIVAVEGYF 180	
DB 121 QRNVQPSIIITAFYQWVSVRNHRSSGSVNTANHTNANAQGLTGTMDYQIVAVEGYF 180	
QY 181 SSGSASITVS 190	
DB 181 SSGSASITVS 190	
RESULT 9	
AAE18495	
ID AAE18495 standard; protein; 190 AA.	
AAE18495;	

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XX 16-MAY-2002 (first entry)
DE Trichoderma reesei xylanase mutant, Trx-161R-162H-165H.
XX
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.
XX
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT MISC-difference 161 /note= "wild type Gln substituted with Arg"
FT MISC-difference 162 /note= "wild type Gln substituted with His"
FT MISC-difference 165 /note= "wild type Thr substituted with His"
FT
FT MISC-difference 165 /note= "wild type Thr substituted with His"
XX
XX WO200192487-A2.
XX
XX 06-DEC-2001.
XX
XX 31-MAY-2001; 2001WO-CA000769.
XX
XX 31-MAY-2000; 2000US-0213803P.
XX
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2002-171435/22.
XX
XX Modified xylanase exhibiting increased thermostability and
XX alkalophilicity useful for industrial processing e.g. for pulp
XX manufacturing.
XX
XX Claim 42; Page; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX useful for bleaching of pulp, processing of precision devices and
XX improving digestibility of poultry and swine feed. Modified xylanase has
XX improved performance at conditions of high temperature and pH and
XX exhibits improved thermostability and/or alkalophilicity in comparison to
XX corresponding native xylanase. The present sequence is Trichoderma reesei
XX xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX specification but is derived from wild type xylanase referred as SEQ ID
XX NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX
XX Sequence 190 AA:
XX
Query Match 95.1%; Score 1014; DB 5; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.5e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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RESULT 10
AA030300
ID AA030300 standard; protein; 190 AA.
XX
XX AA030300;
AC
XX 03-SEP-2003 (first entry)
XX
XX Trichoderma reesei xylanase II mutant protein (S75A).
XX
XX Xylanase; thermostability; alkalophilicity; pulp bleaching; industrial;
XX pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FT MISC-difference 75 /note= "wild type Ser substituted with Ala"
FT
FT WO2003046169-A2.
XX
XX 05-JUN-2003.
XX
XX 20-NOV-2002; 2002WO-CA001758.
XX
XX 21-NOV-2001; 2001US-00990874.
XX
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX
XX WPI; 2003-513647/48.
XX
XX Novel modified xylanase useful in industrial process, exhibits improved
XX thermostability, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native xylanase from Trichoderma reesei.
XX
XX Example 1; Page; 105pp; English.
XX
XX The invention relates to modified xylanase enzyme which exhibits improved
XX thermostability, alkalophilicity and expression efficiency, in comparison
XX to a corresponding native Trichoderma reesei xylanase (Trx). The modified
XX xylanase is useful in an industrial process e.g. pulp manufacturing. It
XX is useful for the bleaching of pulp, processing of precision devices and
XX for improving digestibility of poultry and swine feed. The present
XX sequence is Trichoderma reesei xylanase II mutant protein. Note: This
XX sequence is not shown in the specification but is derived from
XX Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
XX in figure 2 of the specification (AA030259)
XX
XX Sequence 190 AA:
XX
Query Match 95.1%; Score 1014; DB 7; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.5e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```


RESULT 11

AA030303 standard; protein; 190 AA.

AA030303;

03-SEP-2003 (first entry)

Trichoderma reesei xylanase II mutant protein (Q161R).

Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial; KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

Hypocrea jecorina.

Synthetic.

Key Location/Qualifiers

FT Misc-difference 161

/note= "Wild type Gln substituted with Arg"

MO2003046169-A2.

05-JUN-2003.

20-NOV-2002; 2002MO-CA001758.

21-NOV-2001; 2001US-00990874.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

WPI; 2003-513647/48.

Novel modified xylanase useful in industrial process, exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native xylanase from Trichoderma reesei.

Example 1; Page; 105pp; English.

The invention relates to modified xylanase enzyme which exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native Trichoderma reesei xylanase (Trx). The modified

xylanase is useful in an industrial process e.g. pulp manufacturing. It

is useful for the bleaching of pulp, processing of precision devices and

for improving digestibility of poultry and swine feed. The present

sequence is Trichoderma reesei xylanase II mutant protein. Note: This

sequence is not shown in the specification but is derived from

Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16

in figure 2 of the specification (AA030259)

Sequence 190 AA;

Query Match

Best Local Similarity 95.0%; Score 1013; DB 7; Length 190;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Db 181 SSGSASITVS 190

RESULT 12

AA030301 standard; protein; 190 AA.

AA030301;

03-SEP-2003 (first entry)

Trichoderma reesei xylanase II mutant protein (S75G).

Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial; KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

Hypocrea jecorina.

Synthetic.

Key Location/Qualifiers

FT Misc-difference 75

/note= "Wild type Ser substituted with Gly"

MO2003046169-A2.

05-JUN-2003.

20-NOV-2002; 2002MO-CA001758.

21-NOV-2001; 2001US-00990874.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

WPI; 2003-513647/48.

Novel modified xylanase useful in industrial process, exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native xylanase from Trichoderma reesei.

Example 1; Page; 105pp; English.

The invention relates to modified xylanase enzyme which exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native Trichoderma reesei xylanase (Trx). The modified

xylanase is useful in an industrial process e.g. pulp manufacturing. It

is useful for the bleaching of pulp, processing of precision devices and

for improving digestibility of poultry and swine feed. The present

sequence is Trichoderma reesei xylanase II mutant protein. Note: This

sequence is not shown in the specification but is derived from

Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16

in figure 2 of the specification (AA030259)

Sequence 190 AA;

Query Match

Best Local Similarity 95.0%; Score 1013; DB 7; Length 190;
Matches 184; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 181 SSGSASITVS 190

RESULT 12

AA030301 standard; protein; 190 AA.

AA030301;

03-SEP-2003 (first entry)

Trichoderma reesei xylanase II mutant protein (S75G).

Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial; KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.

Hypocrea jecorina.

Synthetic.

Key Location/Qualifiers

FT Misc-difference 75

/note= "Wild type Ser substituted with Gly"

MO2003046169-A2.

05-JUN-2003.

20-NOV-2002; 2002MO-CA001758.

21-NOV-2001; 2001US-00990874.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

WPI; 2003-513647/48.

Novel modified xylanase useful in industrial process, exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native xylanase from Trichoderma reesei.

Example 1; Page; 105pp; English.

The invention relates to modified xylanase enzyme which exhibits improved

thermophilicity, alkalophilicity and expression efficiency, in comparison

to a corresponding native Trichoderma reesei xylanase (Trx). The modified

xylanase is useful in an industrial process e.g. pulp manufacturing. It

is useful for the bleaching of pulp, processing of precision devices and

for improving digestibility of poultry and swine feed. The present

sequence is Trichoderma reesei xylanase II mutant protein. Note: This

sequence is not shown in the specification but is derived from

Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16

in figure 2 of the specification (AA030259)

Sequence 190 AA;

Query Match

Db 181 SSGSASITVS 190

|||||

RESULT 13

AA018647 standard; protein; 190 AA.

ID AAB48541

XX AAB48541;

AC

XX 12-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX

DE Trichoderma reesei xyn II xylanase.

XX

XX Bacterial; Bacillus circulans; xylanase; xylanase activity; XA;

KW bleaching agent.

XX

OS Hypocrea jecorina.

XX

XX WO200068396-A2.

XX

XX 16-NOV-2000.

XX

XX 12-MAY-2000; 2000WO-US013172.

XX

XX 12-MAY-1999; 99US-0133714P.

XX

XX (XENC-) XENCOR INC.

XX

XX Bentzien JM;

XX

XX WPI; 2000-679800/66.

DR

XX

XX Non naturally occurring XA protein with enhanced thermostability,

PT alkalophilicity or thermostability relative to the naturally occurring

PT Bacillus circulans xylanase is used in an agent for bleaching pulp.

XX

XX Disclosure; Fig 16J; 114pp; English.

XX

XX The present sequence is given in a specification relating to non

CC naturally occurring xylanase activity (XA) proteins. The XA proteins

CC comprise an amino acid sequence less than 97% identical to a naturally

CC occurring Bacillus circulans xylanase. They are modified to exhibit

CC enhanced thermostability, alkalophilicity or thermostability relative to

CC the naturally occurring B. circulans xylanase. They may be used as the

CC active compound in a bleaching agent which is used for bleaching pulp.

CC (Updated on 12-SEP-2003 to standardise OS field)

XX

XX

XX Sequence 190 AA;

SC

Query Match 94.9%; Score 1012; DB 3; Length 190;

Best Local Similarity 97.4%; Pred. No. 2.3e-85;

Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TI0PGTGYNNNGYFYSYVNDGHSVYTYNPGGQFSVWMSNSGNFVGKGMOPGTNRKYN 61

Db 2 TI0PGTGYNNNGYFYSYVNDGHSVYTYNPGGQFSVWMSNSGNFVGKGMOPGTNRKYN 61

QY 62 FSGSYNPNKNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSVVDIYRTQ 121

Db 62 FSGSYNPNKNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSVVDIYRTQ 121

QY 122 RVN0PSIIIGTATFYQYWSVRNRHSSGSGVNTACHFNCAHQGLTLGTMDYQIVAVEGYFS 181

Db 122 RVN0PSIIIGTATFYQYWSVRNRHSSGSGVNTACHFNCAHQGLTLGTMDYQIVAVEGYFS 181

QY 182 SSGASITVS 190

Db 182 SSGASITVS 190

RESULT 14

AA018647

ID AA018647 standard; protein; 190 AA.

XX

XX AA018647;

XX

XX 29-AUG-2003 (revised)

DT 24-OCT-2002 (first entry)

XX

XX T reesei xyn II xylanase.

XX

XX Xylanase activity; enzyme; thermostable; xylanase; pulp bleaching;

KW liquid clarification; coffee extraction; plant oil extraction;

KW starch extraction; food thickener; animal food additive; mutant; mutein.

XX

OS Hypocrea jecorina.

XX

XX WO200238746-A2.

XX

XX 16-MAY-2002.

XX

XX 09-NOV-2001; 2001WO-US048018.

XX

XX 10-NOV-2000; 2000US-00710050.

XX

XX (XENC-) XENCOR INC.

XX

XX Bentzien J, Dahlyac B;

XX

XX WPI; 2002-608200/65.

DR

XX

XX Novel xylanase activity protein, useful in bleaching process of pulp and

PT in food and animal feed industry, has enhanced thermostability and

PT alkalophilicity.

XX

XX Disclosure; Fig 16J; 121pp; English.

XX

XX The present invention relates to a non-naturally occurring xylanase

CC activity (XA) protein comprising an amino acid sequence less than 97%

CC identical to a naturally occurring Bacillus circulans xylanase, where the

CC protein has been modified to exhibit enhanced thermostability,

CC alkalophilicity, or thermostability relative to naturally occurring B.

CC circulans xylanase, and has at least 5 amino acid substitutions. A

CC bleaching agent comprising a modified lignocellulosic materials to fuels, for

CC pulp, in the bioconversion of lignocellulosic materials to fuels, for

CC clarifying juice and wine, extracting coffee, plant oils and starch,

CC producing food thickeners, altering texture in bakery products, e.g.

CC improving the quality of dough, helping bread to rise and processing of

CC wheat and corn for starch production, use as animal food additives to aid

CC in the digestibility of feedstuffs and in the washing of super precision

CC devices and semiconductors. The present sequence is a xylanase protein

CC described in the exemplification of the invention. (Updated on 29-AUG-

CC 2003 to standardise OS field)

XX

XX

XX Sequence 190 AA;

SC

Query Match 94.9%; Score 1012; DB 5; Length 190;

Best Local Similarity 97.4%; Pred. No. 2.3e-85;

Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TI0PGTGYNNNGYFYSYVNDGHSVYTYNPGGQFSVWMSNSGNFVGKGMOPGTNRKYN 61

Db 2 TI0PGTGYNNNGYFYSYVNDGHSVYTYNPGGQFSVWMSNSGNFVGKGMOPGTNRKYN 61

QY 62 FSGSYNPNKNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSVVDIYRTQ 121

Db 62 FSGSYNPNKNSYLSVYGMRSNPLIEYIVENFGTYNPGTATKLGECTCDGSVVDIYRTQ 121

QY 122 RVN0PSIIIGTATFYQYWSVRNRHSSGSGVNTACHFNCAHQGLTLGTMDYQIVAVEGYFS 181

Db 122 RVN0PSIIIGTATFYQYWSVRNRHSSGSGVNTACHFNCAHQGLTLGTMDYQIVAVEGYFS 181

QY 182 SSGASITVS 190

Db 182 SSGASITVS 190

Db 182 SGSASITVS 190

Db 181 SSGSASITVS 190

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Job time : 47.5 secs
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RESULT 15

ID	AA030304 standard; protein; 190 AA.
yy	

AC AA030304 ;

DT 03-SEP-2003 (first entry)

DE Trichoderma reesei xylanase II mutant protein (N11D).

KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
KM pulp manufacture; poultry feed; swine feed; enzyme; mutant; muten.

Hypocrea jecorina.

Synthetic

FH	Key	Location/Qualifiers
FF	W1-34660000	1

Misc-difference	11
FT	
FT	/note= "Wild type Asn substituted with Asp"
vv	

PN WO2003046169-A2.

PD 05-JUN-2003.

PF 20-NOV-2002; 2002WO-CA001758.

PR 21-NOV-2001; 2001US-00990874.

PA (CANA) NAT RES COUNCIL CANADA.

PI Sung WL;

DR WPI; 2003-513647/48

Novel modified xylanase useful in industrial process, exhibits improved thermophilicity, alkalophilicity and expression efficiency, in comparison to a corresponding native xylanase from *Trichoderma reesei*.

PS Example 1; Page: 105pp; English.

The invention relates to modified xylanase enzyme which exhibits improved thermostability, alkalophilicity and expression efficiency in comparison to a corresponding native *Trichoderma reesei* xylanase (TrX). The modified xylanase is useful in an industrial process e.g. pulp manufacturing. It is useful for the bleaching of pulp, processing of precision devices and for improving digestibility of poultry and swine feed. The present sequence is *Trichoderma reesei* xylanase II mutant protein. Note: This sequence is not shown in the specification but is derived from *Trichoderma reesei* wild type xylanase II protein shown as SEQ ID NO: 16 in figure 2 of the specification (AA0300259)

Sequence 190 AA;

Query Match	94.9%	Score 1012	DB 7	Length 190
Best Local Similarity	96.8%	Pred. No. 2.3e-85		
Matches 184	Conservative	1	Mismatches 5	Indels 0
				Gaps 0

QY 1 QTTQPQTGVNNCGFYFYSVYNDGAGVATYNNPGGQGVSVNMSNSGNFVGKQKQPTKXVI 60

Db 1 QTTQPQTGVNNCGFYFYSVYNDGAGVATYNNPGGQGVSVNMSNSGNFVGKQKQPTKXVI 60

QY 61 NFGSGYNPNGNSYLSVYGMRSNPPLIEYIVENFGFYNPSTGATKLGECTCDGSPYDIYRT 120

Db 61 NFGSGYNPNGNSYLSVYGMRSNPPLIEYIVENFGFYNPSTGATKLGEFTDSGSPYDIYRT 120

QY 121 QRNVQPSIIIGTATFYQVMSVRNRHSSSGSVNTACHFNCAQHGTLGTMDYQIVAAVEGYF 180

Db 121 QRNVQPSIIIGTATFYQVMSVRNRHSSSGSVNTAHFNMAAQGTLGTMDYQIVAAVEGYF 180

QY 181 SSGSASITVSA 190

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Fri Jul 2 14:30:12 2004

us-09-856-025b-64.ra1

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds

(without alignments)
700.638 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066
Sequence: 1 QTIQPTGNGYNGYPSYND.....YQIYAVEGYPSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 5162571 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A-COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCITUS-COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	95.4	190	1 US-08-044-621D-26	Sequence 26, Appl
2	1017	95.4	190	1 US-08-709-912-16	Sequence 16, Appl
3	1017	95.4	190	2 US-09-047-370-16	Sequence 16, Appl
4	1017	95.4	223	2 US-08-121-436A-2	Sequence 2, Appl
5	1012	94.9	190	4 US-09-570-856B-22	Sequence 22, Appl
6	1007	94.5	190	1 US-08-709-912-17	Sequence 17, Appl
7	1007	94.5	190	2 US-08-047-370-17	Sequence 17, Appl
8	1004	94.2	190	1 US-08-044-621D-27	Sequence 27, Appl
9	1001	93.9	223	3 US-09-254-733-7	Sequence 7, Appl
10	994	93.2	190	4 US-09-570-856B-19	Sequence 19, Appl
11	981	92.0	190	1 US-08-044-621D-28	Sequence 28, Appl
12	981	92.0	190	1 US-08-709-912-14	Sequence 14, Appl
13	981	92.0	190	2 US-08-047-370-14	Sequence 14, Appl
14	975	91.5	190	4 US-09-570-856B-20	Sequence 20, Appl
15	700.5	65.7	261	3 US-08-768-373-2	Sequence 2, Appl
16	700.5	65.7	261	4 US-09-849-242A-2	Sequence 2, Appl
17	652.5	61.2	225	4 US-09-570-856B-26	Sequence 26, Appl
18	647.5	60.7	225	2 US-08-886-765-2	Sequence 2, Appl
19	647.5	60.7	225	2 US-09-115-660-2	Sequence 2, Appl
20	647.5	60.3	194	4 US-09-570-856B-24	Sequence 24, Appl
21	641.5	60.2	225	1 US-08-290-979A-8	Sequence 8, Appl
22	635.5	59.6	194	4 US-09-570-856B-23	Sequence 23, Appl
23	635.5	59.6	230	3 US-08-768-373-4	Sequence 4, Appl
24	635.5	59.6	230	4 US-09-849-242A-4	Sequence 4, Appl
25	633.5	59.4	221	4 US-09-570-856B-29	Sequence 29, Appl
26	631	59.2	226	4 US-09-367-891A-2	Sequence 2, Appl
27	623.5	58.5	223	4 US-09-462-246-2	Sequence 2, Appl

28	612.5	57.5	227	1 US-08-458-023B-4	Sequence 4, Appl
29	606	56.8	231	2 US-08-902-655A-6	Sequence 6, Appl
30	606	56.8	296	1 US-08-507-431-6	Sequence 6, Appl
31	606	56.8	296	3 US-09-116-622-6	Sequence 6, Appl
32	606	56.8	296	3 US-09-219-277-6	Sequence 6, Appl
33	606	56.8	296	3 US-09-599-661-6	Sequence 6, Appl
34	595.5	55.9	189	1 US-08-709-912-13	Sequence 13, Appl
35	595.5	55.9	189	2 US-09-047-370-13	Sequence 13, Appl
36	577.5	54.2	197	1 US-08-044-621D-29	Sequence 29, Appl
37	577.5	54.2	197	1 US-08-709-912-9	Sequence 9, Appl
38	577.5	54.2	197	2 US-09-047-370-9	Sequence 9, Appl
39	577.5	54.2	197	4 US-09-570-856B-18	Sequence 18, Appl
40	574.5	53.9	344	2 US-08-468-812-2	Sequence 2, Appl
41	574.5	53.9	344	4 US-08-590-563-2	Sequence 2, Appl
42	574.5	53.9	344	4 US-09-770-621-2	Sequence 2, Appl
43	574.5	53.9	344	4 US-09-235-832-2	Sequence 2, Appl
44	567	53.2	206	1 US-08-315-695-19	Sequence 19, Appl
45	567	53.2	215	1 US-08-044-621D-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-08-044-621D-26
Sequence 26, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Gowing, Strathly & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Bratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0189
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: NO, 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21KD, pl 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torronene, A., Mach, R. L., Mesener, R.,
AUTHORS: Gonzalez, R., Kalkkinen, N., Harkki, A.
AUTHORS: & Kubicek, C. P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 95.4%; Score 1017; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 9.9e-89;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGNNNGYFYSYNDGHHGVTYTNNGGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
DB 1 QTIOPGTGNNNGYFYSYNDGHHGVTYTNNGGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNGNSYLSYVGMRSNPLIEYIVENFGTYNPSTGATLGECTCGSVYDIYRT 120
DB 61 NFSGSYNPNGNSYLSYVGMRSNPLIEYIVENFGTYNPSTGATLGECTCGSVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQGLTLGTMDOYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQGLTLGTMDOYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2
US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Mesener, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-08-709-912-16

Query Match 95.4%; Score 1017; DB 1; Length 190;
Best Local Similarity 97.4%; Pred. No. 9.9e-89;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGNNNGYFYSYNDGHHGVTYTNNGGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
DB 1 QTIOPGTGNNNGYFYSYNDGHHGVTYTNNGGQFVSVMNSGNTFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNGNSYLSYVGMRSNPLIEYIVENFGTYNPSTGATLGECTCGSVYDIYRT 120
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DB 181 SSGSASITVS 190

RESULT 3
US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr. Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Mach, R. L.
AUTHORS: Messner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 95.4%; Score 1017; DB 2; Length 190;
Best Local Similarity 97.4%; Pred. No. 9.9e-89;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 61 NFSGSYNPNNGSYLSVYGMRSNPLEIYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 120
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Db 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Ritva
APPLICANT: Paloheimo, Marja
APPLICANT: Lantinen, Tarja
APPLICANT: Pajaster m, Richard
TITLE OF INVENTION: No. 5837515 Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbalá, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 95.4%; Score 1017; DB 2; Length 223;
Best Local Similarity 97.4%; Pred. No. 1.2e-88;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGNNGYFYSVYNDGAGVYTNPGGQFSVYMSNSGNFVGGKMGQPGTKNKVI 60
Db 34 QTIQPGTGNNGYFYSVYNDGAGVYTNPGGQFSVYMSNSGNFVGGKMGQPGTKNKVI 93
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Db 94 NFSGSYNPNNGSYLSVYGMRSNPLEIYIVENFGTYNPSTGATKLGECTCDGSVYDIYRT 153
QY 121 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGTMQYQIVAVEGYF 180
Db 154 QRVNOPSIIIGTATFYQYVSVRRNRHSSGSVNTACHFNCAQHGTLTGTMQYQIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 5
US-09-570-856B-22

Sequence 22, Application US/09570856B
Patent No. 6682823
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahljat, Basill I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIORITY APPLICATION NUMBER: US 60/133, 714
PRIORITY FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma reesei
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(1)
OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-22

Query Match 94.9%; Score 1012; DB 4; Length 190;
Best Local Similarity 97.4%; Pred. No. 2,9e-88;
Matches 184; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TTPGTGNNNGYFYSYNDGNGVYTYNGPGQGFVSVMNSGNFVGGKMGQPGTKKVIN 61
DB 2 TTPGTGNNNGYFYSYNDGNGVYTYNGPGQGFVSVMNSGNFVGGKMGQPGTKKVIN 61
QY 62 FSGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNSTGATKLGECTCGSYVDIYRTQ 121
DB 62 FSGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNSTGATKLGECTCGSYVDIYRTQ 121
QY 122 RVNOPSITIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYFS 181
DB 122 RVNOPSITIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYFS 181
QY 182 SSGSASITVS 190
DB 182 SSGSASITVS 190

RESULT 6
US-08-709-912-17
Sequence 17, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermostability, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujie, M
AUTHORS: Watson, D. C.
AUTHORS: Makarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-08-709-912-17

Query Match 94.5%; Score 1007; DB 1; Length 190;
Best Local Similarity 96.3%; Pred. No. 8,8e-88;
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQGTGNNNGYFYSYNDGNGVYTYNGPGQGFVSVMNSGNFVGGKMGQPGTKKVI 60
DB 1 QTIQGTGNNNGYFYSYNDGNGVYTYNGPGQGFVSVMNSGNFVGGKMGQPGTKKVI 60
QY 61 NFSGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNSTGATKLGECTCGSYVDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGKSRNPLIEYIVENFGTYNSTGATKLGECTCGSYVDIYRT 120
QY 121 QRVNOPSITIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYF 180
DB 121 QRVNOPSITIGTATFYQYMSVRRNRHSSGGSVNTACHFNCAOHGLTLGMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermostability, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047.370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olisen M., Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujile, M
AUTHORS: Watson, D. C.
AUTHORS: Makarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 94.5%; Score 1007; DB 2; Length 190;
Best Local Similarity 96.3%; Pred. No. 8.8e-88;
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDSHGCVTYTNGPGQPSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 QTIQPGTGYNNGYFYSYWNDSHGCVTYTNGPGQPSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPSTGATYKLGECTCDGSGVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPSTGATYKLGECTCDGSGVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGLTLGTMQYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGLTLGTMQYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8
US-08-044-621D-27
Sequence 27, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yasuchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:

ADDRESSEE: Gowling, Strachy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1G3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Strate
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: No
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
STRAIN: Trichoderma viride, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Ujile M., Watson
AUTHORS: D.C., & Makarchuk W.
TITLE: Amino Acid Sequence of the Low-Molecular-
TITLE: Weight Xylanase from Trichoderma viride
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 149-154
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-27

Query Match 94.2%; Score 1004; DB 1; Length 190;
Best Local Similarity 95.8%; Pred. No. 1.7e-87;
Matches 182; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDSHGCVTYTNGPGQPSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 QTIQPGTGYNNGYFYSYWNDSHGCVTYTNGPGQPSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPSTGATYKLGECTCDGSGVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSVYGMSRNPLEYIYVENFGTYNPSTGATYKLGECTCDGSGVYDIYRT 120
QY 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGLTLGTMQYQIVAVEGYF 180
DB 121 QRVNOPSIIIGTATFYQYWSVRRNRSSGSVNTACHFNCAOHGLTLGTMQYQIVAVEGYF 180

Db 121 QVNPSTIGTATFYQVWSVRNRSSGSVNTANHFNAQOGLTLGTMDOIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 9

US-09-254-733-7
 ; Sequence 7, Application US/09254733
 ; Patent No. 6277596
 ; GENERAL INFORMATION:
 ; APPLICANT: WATANABE, MANABU
 ; APPLICANT: MORIYA, TATSUKI
 ; APPLICANT: AOYAGI, KAORI
 ; APPLICANT: SUMIDA, NAOMI
 ; APPLICANT: MURAKAMI, TAKESHI
 ; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULASE CBH1 GENES ORIGINATING
 ; TITLE OF INVENTION: IN TRICODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
 ; FILE REFERENCE: 99-0266*/LC(MMC)/00144
 ; CURRENT FILING DATE: 1999-05-07
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: TRICODERMA VIRIDE MC300-1
 US-09-254-733-7

Query March 93.9%; Score 1001; DB 3; Length 223;
 Best Local Similarity 95.3%; Pred. No. 4e-87; 7; Indels 0; Gaps 0;
 Matches 181; Conservative 2; Mismatches

QY 1 OTIOPGTGYNNGYFYSYNDGHSYTYTNGPGGQFSYVWNSGNGFVGKGMQPGTKXKI 60
 Db 34 OTIOPGTGYNNGYFYSYNDGHSYTYTNGPGGQFSYVWNSGNGFVGKGMQPGTKXKI 93
 QY 61 NFSGTYPNNGNSYLSYVGWMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120
 Db 94 NFSGTYPNNGNSYLSYVGWMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 153
 QY 121 QVNPSTIGTATFYQVWSVRNRSSGSVNTACHFNCMAOGLTLGTMDOIVAVEGYF 180
 Db 154 QVNPSTIGTATFYQVWSVRNRSSGSVNTANHFNAQOGLTLGTMDOIVAVEGYF 213
 QY 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 10

US-09-570-856B-19
 ; Sequence 19, Application US/09570856B
 ; Patent No. 6682923
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentzien, Joerg M
 ; APPLICANT: Dahlvat, Bassil I
 ; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
 ; FILE REFERENCE: A-67478-1/PRT/RMS/RMK
 ; CURRENT FILING DATE: 2002-04-15
 ; PRIOR APPLICATION NUMBER: US 60/133, 714
 ; PRIOR FILING DATE: 1999-05-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Trichoderma viride
 US-09-570-856B-19

Query March 93.2%; Score 994; DB 4; Length 190;
 Best Local Similarity 94.7%; Pred. No. 1.5e-86;
 Matches 180; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTIOPGTGYNNGYFYSYNDGHSYTYTNGPGGQFSYVWNSGNGFVGKGMQPGTKXKI 60
 Db 1 OTIOPGTGYNNGYFYSYNDGHSYTYTNGPGGQFSYVWNSGNGFVGKGMQPGTKXKI 60
 QY 61 NFSGTYPNNGNSYLSYVGWMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120
 Db 61 NFSGTYPNNGNSYLSYVGWMSRNPLEYIYVENFGTNPSTGATLGECTDGSVYDIYRT 120
 QY 121 QVNPSTIGTATFYQVWSVRNRSSGSVNTACHFNCMAOGLTLGTMDOIVAVEGYF 180
 Db 121 QVNPSTIGTATFYQVWSVRNRSSGSVNTANHFNAQOGLTLGTMDOIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 11

US-08-044-621D-28
 ; Sequence 28, Application US/08044621D
 ; Patent No. 5405769
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren W. Makarchuk
 ; APPLICANT: Wang L. Sung
 ; APPLICANT: Makoto Yaguchi
 ; APPLICANT: Robert L. Campbell
 ; APPLICANT: David R. Rose
 ; TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
 ; TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Gowing, Strachy & Henderson
 ; STREET: Suite 2600, 160 Elgin Street
 ; CITY: Ottawa
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: K1P 1G3
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
 ; COMPUTER: IBM PC
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/044,621D
 ; FILING DATE: April 8, 1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Judy A. Erratt
 ; REGISTRATION NUMBER: 34,076
 ; REFERENCE/DOCKET NUMBER: 08-863796
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 613-786-0199
 ; TELEFAX: 613-563-9869
 ; TREEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 190
 ; TYPE: Amino Acid
 ; STRANDEDNESS: No. 5405769 Relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:
 ; DESCRIPTION: protein
 ; HYPOTHETICAL: No
 ; ANTI-SENSE: No
 ; FRAGMENT TYPE: No
 ; ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum
 STRAIN: Trichoderma harzianum, 20Xd
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
 AUTHORS: F., Tan L.U.L., Senior D.J., & Saddler
 AUTHORS: J.N.
 TITLE:
 JOURNAL: Xylans and Xylanases
 VOLUME:
 ISSUE:
 PAGES: 435-438
 DATE: 1992
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-28

Query Match 92.0%; Score 981; DB 1; Length 190;
 Best Local Similarity 93.2%; Pred. No. 2.5e-85;
 Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 Db 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGTYNPSTGATKLGECTCDGSGVYDIYRT 120
 Db 61 NFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGTYNPSTGATKLGECTCDGSGVYDIYRT 120
 QY 121 QRVNOPSITGATFYQWYSVRNRHSSGSVNTACHFNCKACHGLTLGTMQYQIVAVEGYF 180
 Db 121 QRVNOPSITGATFYQWYSVRNRHSSGSVNTACHFNCKACHGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 12
 US-08-709-912-14
 ; Sequence 14, Application US/08709912
 ; Patent No. 5759840
 ; GENERAL INFORMATION:
 ; APPLICANT: Sung Dr., Wing L
 ; APPLICANT: Yaguchi Dr., Makoto
 ; APPLICANT: Ishikawa Dr., Kazuhiko
 ; TITLE OF INVENTION: Modification of xylanase to improve
 ; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 ; STREET: 277 Park Ave.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10172-0194
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/709,912
 ; FILING DATE: 09-SEP-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Olsen Mr, Warren E
 ; REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma harzianum
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi, M
 AUTHORS: Roy, C
 AUTHORS: Watson, D. C.
 AUTHORS: Rollin, F
 AUTHORS: Tan, L. U. L.
 AUTHORS: Senior, D. J.
 AUTHORS: Saddler, J. N.
 JOURNAL: Xylan and Xylanase
 PAGES: 435-438
 DATE: 1992
 US-08-709-912-14

Query Match 92.0%; Score 981; DB 1; Length 190;
 Best Local Similarity 93.2%; Pred. No. 2.5e-85;
 Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 Db 1 QTIQPGTGYNNNGYFYSYWMDHGGVYTYNGPGQFQSVNWSNNGNFVGGKMGQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGTYNPSTGATKLGECTCDGSGVYDIYRT 120
 Db 61 NFSGSYNPNNGNSYLSVYGMNRNPLIEYIVENFGTYNPSTGATKLGECTCDGSGVYDIYRT 120
 QY 121 QRVNOPSITGATFYQWYSVRNRHSSGSVNTACHFNCKACHGLTLGTMQYQIVAVEGYF 180
 Db 121 QRVNOPSITGATFYQWYSVRNRHSSGSVNTACHFNCKACHGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 13
 US-09-047-370-14
 ; Sequence 14, Application US/09047370
 ; Patent No. 5866408
 ; GENERAL INFORMATION:
 ; APPLICANT: Sung Dr., Wing L
 ; APPLICANT: Yaguchi Dr., Makoto
 ; APPLICANT: Ishikawa Dr., Kazuhiko
 ; TITLE OF INVENTION: Modification of xylanase to improve
 ; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 ; STREET: 277 Park Ave.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10172-0194
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039, 2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Thrichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yasuchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. J.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-09-047-370-14

Query Match 92.0%; Score 981; DB 2; Length 190;
Best Local Similarity 93.2%; Pred. No. 2.5e-85;
Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIPTGTGNNNGYFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 60
DB 1 QTIPTGTGNNNGYFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 60
QY 61 NFSGSYNNGNSYLSYVGSWSPNPLEYIYVENFGTYPSTGATKLGCTCDGSGVYDIYRT 120
DB 61 NFSGSYNNGNSYLSYVGSWSPNPLEYIYVENFGTYPSTGATKLGCTCDGSGVYDIYRT 120
QY 121 QRVNPSIIGTATFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180
DB 121 QRVNPSIIGTATFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 14
US-09-570-856B-20
Sequence 20, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Bentzien, Joerg M
APPLICANT: Dahlvat, Baasil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133, 714

PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma harzianum
US-09-570-856B-20

Query Match 91.5%; Score 975; DB 4; Length 190;
Best Local Similarity 92.6%; Pred. No. 9.3e-65;
Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIPTGTGNNNGYFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 60
DB 1 QTIPTGTGNNNGYFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 60
QY 61 NFSGSYNNGNSYLSYVGSWSPNPLEYIYVENFGTYPSTGATKLGCTCDGSGVYDIYRT 120
DB 61 NFSGSYNNGNSYLSYVGSWSPNPLEYIYVENFGTYPSTGATKLGCTCDGSGVYDIYRT 120
QY 121 QRVNPSIIGTATFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180
DB 121 QRVNPSIIGTATFYQVWSVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 15
US-08-768-373-2
Sequence 2, Application US/08768373
Patent No. 6228629
GENERAL INFORMATION:
APPLICANT: PALOHEIMO, MARJA
APPLICANT: HAKOLA, SATU
APPLICANT: M NTYL, ARJA
APPLICANT: VERMAANPER, JARI
APPLICANT: LANTTO, RAISA
APPLICANT: LAHTINEN, TARJA
APPLICANT: FAGERSTR M, RICHARD
APPLICANT: SUOMINEN, PIIRKO
TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768, 373
FILING DATE: 17-DEC-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008, 746
FILING DATE: 18-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020, 839
FILING DATE: 28-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: CIMEALA, MICHELE A.
REGISTRATION NUMBER: 33, 851
REFERENCE/DOCKET NUMBER: 1050, 0540003
TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (202) 371-2600
 / TELEFAX: (202) 371-2540
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 261 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / ORIGINAL SOURCE:
 / ORGANISM: Chaetomium thermophilum
 / STRAIN: CBS730.95
 / FEATURE:
 / NAME/KEY: Protein
 / LOCATION: 1..261
 / OTHER INFORMATION: /label= XLNA
 US-08-768-373-2

Query Match 65.7%; Score 700.5; DB 3; Length 261;
 Best Local Similarity 64.2%; Pred. No. 1.3e-58;
 Matches 122; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY	1	QTI-QPGGYNNGYFYSYMNDGHHGVTYTNQPGGQPSVMSNSGNEFYGKMQPGTKNKY	59
DB	27	QTLTSSATGTHNGYYSFMTDGGNIRFNLESGGQISVTMSGNMGVGGKNNPGTDNRV	86
QY	60	INFGSYNPNNGNSYLSYVGWSRNPFLIEYIVENFGTYNPSGTATKLGECTDGSVYDIYR	119
DB	87	INYADYRPNNGNSYLAAYGWTNRNPLIEYVYESFGTYDPSTGATRMGSVTTDGGTYNIYR	146
QY	120	TORVNPSSITGATFYQYWSVRNRHSSGSVNTACHENCWAQGLTGTMDYQIVAVEGY	179
DB	147	TORVNPSSITGATFYQYWSVRNRHSSGSVNTACHENCWAQGLTGTMDYQIVAVEGY	206
QY	180	FSSGSASITV	189
DB	207	YSSGSATVNV	216

Search completed: June 30, 2004, 19:44:48
 Job time : 15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds
(without alignments)
1441.987 Million cell updates/sec

Title: US-09-856-025B-64
Perfect score: 1066
Sequence: 1 QTIQPTGYNNGYFYSYWMD.....YQIVAVEGYSGSGASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1166195 seqs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	190	US-10-307-441-16	Sequence 16, Appl
2	1017	95.4	222	US-10-237-386-32	Sequence 16, Appl
3	1017	95.4	222	US-10-237-386-31	Sequence 31, Appl
4	1007	94.5	190	US-10-307-441-17	Sequence 17, Appl
5	1005	94.3	223	US-10-237-386-30	Sequence 30, Appl
6	981	92.0	190	US-10-307-441-14	Sequence 14, Appl
7	975	91.5	190	US-10-237-386-33	Sequence 33, Appl
8	860	80.7	223	US-10-237-386-34	Sequence 34, Appl
9	755.5	70.9	241	US-10-237-386-35	Sequence 35, Appl
10	695.5	65.2	219	US-10-237-386-29	Sequence 29, Appl
11	667.5	62.6	227	US-10-237-386-22	Sequence 22, Appl
12	661.5	62.1	227	US-10-237-386-21	Sequence 21, Appl
13	661	62.0	233	US-10-213-990-72	Sequence 72, Appl
14	654.5	61.4	234	US-10-213-990-69	Sequence 69, Appl
15	647.5	60.7	189	US-10-307-441-19	Sequence 19, Appl

16	647.5	60.7	194	US-10-307-441-20	Sequence 20, Appl
17	647.5	60.7	225	US-09-467-368-2	Sequence 2, Appl
18	647.5	60.7	225	US-10-237-386-24	Sequence 24, Appl
19	645.5	60.6	221	US-10-213-990-66	Sequence 66, Appl
20	640.5	60.1	225	US-10-237-386-36	Sequence 36, Appl
21	633.5	59.4	221	US-10-237-386-20	Sequence 20, Appl
22	632	59.3	223	US-10-237-386-37	Sequence 37, Appl
23	623.5	58.5	223	US-10-299-393-2	Sequence 2, Appl
24	623	58.4	231	US-09-790-070A-11	Sequence 11, Appl
25	622.5	58.4	231	US-10-237-386-26	Sequence 26, Appl
26	615.5	57.7	231	US-10-237-386-25	Sequence 25, Appl
27	606.5	56.9	227	US-10-237-386-27	Sequence 27, Appl
28	605.5	56.8	221	US-10-237-386-44	Sequence 44, Appl
29	595.5	55.9	189	US-10-307-441-13	Sequence 13, Appl
30	595.5	55.9	240	US-10-237-386-42	Sequence 42, Appl
31	594.5	55.8	239	US-10-237-386-40	Sequence 40, Appl
32	593.5	55.7	241	US-10-237-386-43	Sequence 43, Appl
33	587	55.1	216	US-10-237-386-45	Sequence 45, Appl
34	578	54.2	228	US-10-237-386-39	Sequence 39, Appl
35	577.5	54.2	197	US-10-307-441-9	Sequence 9, Appl
36	577.5	54.2	201	US-10-237-386-23	Sequence 23, Appl
37	574.5	53.9	344	US-09-770-621-2	Sequence 2, Appl
38	574.5	53.9	344	US-10-286-993-2	Sequence 2, Appl
39	569.5	53.4	242	US-10-237-386-41	Sequence 41, Appl
40	565	53.0	191	US-10-307-441-10	Sequence 10, Appl
41	559.5	52.5	233	US-10-237-386-28	Sequence 28, Appl
42	519.5	48.7	237	US-10-237-386-47	Sequence 47, Appl
43	514.5	48.3	226	US-10-237-386-63	Sequence 63, Appl
44	511.5	48.0	232	US-10-237-386-64	Sequence 64, Appl
45	509.5	47.8	236	US-10-237-386-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1	
US-10-307-441-16	
Sequence 16, Application US/10307441	
Publication No. US20030166236A1	
GENERAL INFORMATION:	
APPLICANT: SUNG, Wing L.	
TITLE OF INVENTION: National Research Council of Canada	
TITLE OF INVENTION: Modified xylanase Exhibiting Increased Thermophilicity	
FILE REFERENCE: 027367-5006US	
CURRENT APPLICATION NUMBER: US/10/307,441	
PRIOR FILING DATE: 2002-12-02	
PRIOR APPLICATION NUMBER: PCT/CA01/00769	
PRIOR FILING DATE: 2001-05-31	
PRIOR APPLICATION NUMBER: 60/213,803	
PRIOR FILING DATE: 2000-05-31	
NUMBER OF SEQ ID NOS: 51	
SOFTWARE: Patent In Ver. 2.1	
SEQ ID NO 16	
LENGTH: 190	
TYPE: PRT	
ORGANISM: Trichoderma reesei	
US-10-307-441-16	
Query Match	95.4%; Score 1017; DB 14; Length 190;
Best Local Similarity	97.4%; Pred. No. 1.3e-92;
Matches 185; Conservative	0; Mismatches 5; Indels 0; Gaps 0;
QY	1 QTIQCTGYNNGYFYSYWMDGGVTTNNGGCGFSVWWSNGNFGAKGQPGTKNKVI 60
DB	1 QTIQCTGYNNGYFYSYWMDGGVTTNNGGCGFSVWWSNGNFGAKGQPGTKNKVI 60
QY	61 NFSGSYNNGSYLVGWSRNPLEYIVENFGTYNSTGATKLGECTCGSVYDIYRT 120
DB	61 NFSGSYNNGSYLVGWSRNPLEYIVENFGTYNSTGATKLGECTCGSVYDIYRT 120
QY	121 QRVNPSIIIGTATFQGVSVRRNRSSGVNTACIFNKWAQGLTLMYQIVAVEGYF 180

Db 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTANHFNAQAQGLTLGTMDOYIIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 2
US-10-237-386-32
Sequence 32, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2002-12-06
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 32
LENGTH: 222
TYPE: PRT
ORGANISM: T. reesei
US-10-237-386-32

Query Match 95.4%; Score 1017; DB 14; Length 222;
Best Local Similarity 97.4%; Pred. No. 1.6e-92;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 60
Db 33 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 92
QY 61 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 120
Db 93 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 152
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 180
Db 153 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 212
QY 181 SSGSASITVS 190
Db 213 SSGSASITVS 222

RESULT 3
US-10-237-386-31
Sequence 31, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2002-12-06
CURRENT APPLICATION NUMBER: US/10/237,386
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
NUMBER OF SEQ ID NOS: 66

SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 223
TYPE: PRT
ORGANISM: T. reesei
US-10-237-386-31

Query Match 95.4%; Score 1017; DB 14; Length 223;
Best Local Similarity 97.4%; Pred. No. 1.6e-92;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 60
Db 34 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 93
QY 61 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 120
Db 94 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 153
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 180
Db 154 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 4
US-10-307-441-17
Sequence 17, Application US/10307441
Publication No. US20030166236A1
GENERAL INFORMATION:
APPLICANT: SUNG, Wang L.
TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
FILE REFERENCE: 027367-5006US
CURRENT FILING DATE: 2002-12-02
CURRENT APPLICATION NUMBER: US/10/307,441
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: PCT/CA01/00769
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 60/213,803
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma viride
US-10-307-441-17

Query Match 94.5%; Score 1007; DB 14; Length 190;
Best Local Similarity 96.3%; Pred. No. 1.3e-91;
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 60
Db 1 QTIQPGTGYNNGYFYSYWNDGHSVYTNNGPGQFSVWMSNSGNFVGKGMQPGTKXKVI 60
QY 61 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 120
Db 61 NFSGSYNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPGTATGCTCGSDGYVDIYRT 120
QY 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 180
Db 121 QRVNPSIIGTATFYQYWSVRNRHSSGSVNTACHFNCAQHGTLGTMDOYIIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 5
US-10-237-386-30

; Sequence 30, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-30

Query Match 94.3%; Score 1005; DB 14; Length 223;
Best Local Similarity 96.3%; Pred. No. 2,4e-91;
Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 34 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 93
QY 61 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 120
DB 94 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 153
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 180
DB 154 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

RESULT 6
US-10-307-441-14

; Sequence 14, Application US/10307441
; Publication No. US2003016236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match 92.0%; Score 981; DB 14; Length 190;
Best Local Similarity 93.2%; Pred. No. 4,8e-89;

Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 120
DB 61 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 7
US-10-237-386-33

; Sequence 33, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRT
; ORGANISM: T. harzianum
US-10-237-386-33

Query Match 91.5%; Score 975; DB 14; Length 190;
Best Local Similarity 92.6%; Pred. No. 1,9e-88;
Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
DB 1 QTIQPGTYNNGYFYSYWMDGHGVTYTNPGGQFSVWMSNSGNFVGKMGQPGTKNKVI 60
QY 61 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 120
DB 61 NFGSYNPNNGSYLSYVGSWRNPLIEYIVENFGTNPSTGATKLGECTCDDSVYDIYRT 120
QY 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 180
DB 121 QRVNPSIIIGTATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTLGTMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8
US-10-237-386-34

; Sequence 34, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole

```

; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. viride
US-10-237-386-34

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Query Match      80.7%; Score 860; DB 14; Length 223;
Best Local Similarity 80.5%; Pred. No. 5,5e-77;
Matches 153; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

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QY 1 QTIQPGTGYNNGYFYSYWNDHGCVTYTNGPGQPSYVNSGNYFVGKGMQPTKXKI 60
DB 34 QTIQPGTGFNNGYFYSYWNDHGSGVTYTNGAGSFSYVWNSGNFVGKGMNPGSSSVI 93
QY 61 NFGSYVNSGNYFYSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRT 120
DB 94 NFGSYVNSGNYFYSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRT 153
QY 121 QRVNPSIIGTATFYQYVSVRRNRSSGSVNTACHFNCMAQHLTGTMDOYQVAVEGYF 180
DB 154 QRVNPSIIGTATFYQYVSVRRNRHAPARSRRLRTTSNANMLGTLGTLDOYQVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGNANITVS 223

```

```

RESULT 9
US-10-237-386-35
; Sequence 35, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 241
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-35

```

```

Query Match      70.9%; Score 755.5; DB 14; Length 241;
Best Local Similarity 72.7%; Pred. No. 1.4e-66;
Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

```

```

QY 7 TGYNNGYFYSYWNDHGCVTYTNGPGQPSYVNSGNYFVGKGMQPTKXKIYVNSGSY 66
DB 38 TGYNNGYFYSWTDGQGNQVYTNAGQGYVTVWNSGNFVGKGMNPGSA-RTINITYAN 96

```

```

QY 67 NFGNSYLSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRTQVNP 126
DB 97 NFGNSYLSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRTQVNP 156
QY 127 SIIGTATFYQYVSVRRNRSSGSVNTACHFNCMAQHLTGTMDOYQVAVEGYFSSGSA 186
DB 157 SIIGTATFYQYVSVRRNRSSGSVNTACHFNCMAQHLTGTMDOYQVAVEGYFSSGSA 216
QY 187 ITV 189
DB 217 VNV 219

```

```

RESULT 10
US-10-237-386-29
; Sequence 29, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 219
; TYPE: PRT
; ORGANISM: C. gracile
US-10-237-386-29

```

```

Query Match      65.2%; Score 695.5; DB 14; Length 219;
Best Local Similarity 67.6%; Pred. No. 1.1e-60;
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

```

```

QY 6 GTGYNNGYFYSYWNDHGCVTYTNGPGQPSYVNSGNYFVGKGMQPTKXKIYVNSGS 65
DB 36 GTGYNNGYFYSWTDGQGNQVYTNAGQGYVTVWNSGNFVGKGMNPGSA-RTINITYAN 94
QY 66 YNPNNSYLSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRTQVNP 125
DB 95 YNPNNSYLSYVWNSGNPLIEYIYVENFGTYNPGATKLGCTCDGSGVYDIYRTQVNP 154
QY 126 SIIGTATFYQYVSVRRNRSSGSVNTACHFNCMAQHLTGTMDOYQVAVEGYFSSGSA 185
DB 155 SIIGTATFYQYVSVRRNRSSGSVNTACHFNCMAQHLTGTMDOYQVAVEGYFSSGSA 214
QY 186 SITVS 190
DB 215 SITVS 219

```

```

RESULT 11
US-10-237-386-22
; Sequence 22, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; CURRENT FILING DATE: 2002-12-06

```

PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 227
TYPE: PRT
ORGANISM: A. pisi
US-10-237-386-22

Query Match 62.6%; Score 667.5; DB 14; Length 227;
Best Local Similarity 64.2%; Pred. No. 6.5e-58;
Matches 124; Conservative 20; Mismatches 44; Indels 5; Gaps 2;

QY 2 TIDPQT---GYNNGYFYSYNDHGGVYTNNGPQGFVSVMWSNGFVGKGMQPGTKN 57
DB 34 TAAAGTBSQGTHTGCTFYSMTDGAQATYTNNGAGSYVMKTKGSLVGGKGNPGAA- 92
QY 58 KVINFGSYNDPNSYLSVYGSNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 117
DB 93 RTITYSGTSPSGNSYLAIVGWTNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 152
QY 118 YRTORVNPSTIGTATFYQVSVRNRHSSGSVNTACHFNCAOHGLTGLTMDYQIVAVE 177
DB 153 AQTPTNPSTIDGTQYTFQYVSVRNRHSSGSVNMKTHFPAWAKMKLGCTHNYQIVATE 212
QY 178 GFSSGSASITVS 190
DB 213 GFSSGSASITVN 225

RESULT 12
US-10-237-386-21
Sequence 21, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sidsesen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 227
TYPE: PRT
ORGANISM: H. turcicum
US-10-237-386-21

Query Match 62.1%; Score 661.5; DB 14; Length 227;
Best Local Similarity 63.2%; Pred. No. 2.6e-57;
Matches 120; Conservative 22; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIOPGTGYNNGYFYSYNDHGGVYTNNGPQGFVSVMWSNGFVGKGMQPGTKN 60
DB 37 QSTNGSGTNGCTYSWMSDGAARATYTNNGAGSYVMKTKGSLVGGKGNPGAA- 95
QY 61 NFGSGYNDPNSYLSVYGSNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 120
DB 96 TYSQYNDPNSYLAIVGWTNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 155

QY 121 QRVNPSTIGTATFYQVSVRNRHSSGSVNTACHFNCAOHGLTGLTMDYQIVAVE 180
DB 156 TRINQSIDGTTRFQYVSVRNRHSSGSVNMKTHFPAWAKMKLGCTHNYQIVATE 215
QY 181 SSGSASITVS 190
DB 216 SSGSASITVN 225

RESULT 13
US-10-213-990-72
Sequence 72, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 313
TYPE: PRT
ORGANISM: Aspergillus
US-10-213-990-72

Query Match 62.0%; Score 661; DB 14; Length 313;
Best Local Similarity 62.2%; Pred. No. 4.3e-57;
Matches 120; Conservative 29; Mismatches 40; Indels 4; Gaps 3;

QY 1 QTIOPG-TGYNNGYFYSYNDHGGVYTNNGPQGFVSVMWS--NSGNFVGKGMQPGTKN 57
DB 32 QTIITTSQGTNNGYYSFMTNGAGSYQYTNNGAGSYVTWANQNGDFTGKGMNPGSDH 91
QY 58 KVINFGSYNDPNSYLSVYGSNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 117
DB 92 D-ITTSFSPSGNSYLAIVGWTNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 150
QY 118 YRTORVNPSTIGTATFYQVSVRNRHSSGSVNTACHFNCAOHGLTGLTMDYQIVAVE 177
DB 151 YHQYNDPNSYLAIVGWTNPLIEYIVENFGTYNPGTATKLGECTCDGSVYDI 210
QY 178 GFSSGSASITVS 190
DB 211 GFSSGSASITVN 223

RESULT 14
US-10-213-990-69
Sequence 69, Application US/10213990
Publication No. US20030082595A1
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Storms, Reg
APPLICANT: Roemer, Terry
TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUNIGATUS ENCODING INDUSTRIAL
FILE REFERENCE: 10182-019-999
CURRENT APPLICATION NUMBER: US/10/213,990
CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 69
LENGTH: 234
TYPE: PRT
ORGANISM: Aspergillus
US-10-213-990-69

Query Match	61.4%;	Score 654.5;	DB 14;	Length 234;
Best Local Similarity	61.7%;	Pred. No. 1,3e-56;		
Matches 116;	Conservative 24;	Mismatches 43;	Indels 5;	Gaps 11

[illegible]

RESULT 15
 US-10-307-441-19
 : Sequence 19, Application US/10307441
 : Publication No. US20030166236A1
 : GENERAL INFORMATION:
 : APPLICANT: SUNG, Ming L.
 : APPLICANT: National Research Council of Canada
 : TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity
 : TITLE OF INVENTION: and Alkalophilicity
 : FILE REFERENCE: 027367-5006US
 : CURRENT APPLICATION NUMBER: US/10/307,441
 : CURRENT FILING DATE: 2002-12-02
 : PRIOR APPLICATION NUMBER: PCT/CA01/00769
 : PRIOR FILING DATE: 2001-05-31
 : PRIOR APPLICATION NUMBER: 60/213,803
 : PRIOR FILING DATE: 2000-05-31
 : NUMBER OF SEQ ID NOS: 51
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 19
 : LENGTH: 189
 : TYPE: PRT
 : ORGANISM: Aspergillus awamori
 : US-10-307-441-19

Query Match	60.7%;	Score 647.5;	DB 14;	Length 189;
Best Local Similarity	63.4%;	Pred. No. 5e-56;		
Matches 116;	Conservative 23;	Mismatches 43;	Indels 1;	Gaps 1

```

QY      67  NPNGNSLSTVYGMSSRNPLEYYIVENFGFTYBPTGATKLGECTCDGSVYDIYFQVRVNP 125
Db      66  TPGSNGLSTVYGMWTTDPLIEYYIVESYGDYXNPQSGGTTGRNVSSDGSVYDIYATRTAP 124
QY      127  SIIETAFFIYQWYSIRRHRRSSGSVNTACHFNCAHQGLLTGMDQIYAVAGYTSSSGAS 186
Db      126  SIDETQTFQSYWYSRQKRFVGTFTVTSNHNMAWAKLGNLTGHNPQILATIGYQSSGSSS 185
QY      187  ITV 189
Db      186  ITI 188

```

Search completed: June 30, 2004, 19:59:13
Job time : 38.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:39 ; Search time 13 Seconds

(without alignments)
1405.876 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066

Sequence: 1 QTIOPGTGNNGYFYSTYWD.....YQIVAVEGFGSSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.78:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

6: PIR5:*

7: PIR6:*

8: PIR7:*

9: PIR8:*

10: PIR9:*

11: PIR10:*

12: PIR11:*

13: PIR12:*

14: PIR13:*

15: PIR14:*

16: PIR15:*

17: PIR16:*

18: PIR17:*

20: PIR18:*

21: PIR19:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	95.4	222	S39154	xylinase 1 - fungus
2	1017	95.4	222	S39883	endo-1,4-beta-xylinase
3	994	93.2	190	A44594	endo-1,4-beta-xylinase
4	990	92.9	190	A44595	endo-1,4-beta-xylinase
5	981	92.0	190	A44593	endo-1,4-beta-xylinase
6	755.5	70.9	241	S71473	endo-1,4-beta-xylinase
7	695.5	65.2	219	S71472	endo-1,4-beta-xylinase
8	681.5	63.9	232	UC7577	endo-1,4-beta-xylinase
9	660.5	62.0	225	S57477	endo-1,4-beta-xylinase
10	649.5	60.9	221	S57469	endo-1,4-beta-xylinase
11	632	59.3	221	UC7307	endo-1,4-beta-xylinase
12	606.5	56.9	227	S43919	endo-1,4-beta-xylinase
13	577.5	54.2	197	A44597	endo-1,4-beta-xylinase
14	567	53.2	333	JS0590	endo-1,4-beta-xylinase
15	567	53.2	335	TS0601	endo-1,4-beta-xylinase
16	550.5	51.6	644	I40712	endo-1,4-beta-xylinase
17	519.5	48.7	661	S59633	endo-1,4-beta-xylinase
18	509.5	47.8	666	S59631	endo-1,4-beta-xylinase
19	506.5	47.5	241	TS0705	endo-1,4-beta-xylinase
20	503	47.2	240	JS0591	endo-1,4-beta-xylinase
21	501	47.0	240	S47512	endo-1,4-beta-xylinase
22	500.5	47.0	210	C83762	endo-1,4-beta-xylinase
23	488	45.8	213	I40569	endo-1,4-beta-xylinase
24	487	45.7	213	SC1734	endo-1,4-beta-xylinase
25	487	45.7	213	S48126	endo-1,4-beta-xylinase
26	486	45.7	213	WBSXP	endo-1,4-beta-xylinase
27	456	43.8	354	S51779	endo-1,4-beta-xylinase
28	441.5	41.4	261	S12745	endo-1,4-beta-xylinase
29	430	40.3	511	JO1935	endo-1,4-beta-xylinase

30	422.5	39.6	209	UC4909	endo-1,4-beta-xylinase
31	419	39.3	211	S48229	endo-1,4-beta-xylinase
32	418.5	39.3	229	S39155	xylinase 2 - fungus
33	417	39.1	211	S49542	endo-1,4-beta-xylinase
34	414	38.8	211	UC1198	endo-1,4-beta-xylinase
35	388	36.4	954	S20907	endo-1,4-beta-xylinase
36	382	35.8	789	S58235	endo-1,4-beta-xylinase
37	375.5	35.2	802	A36910	xylinase, beta(1,3)
38	373	35.0	781	S51592	xylinase precursor - R
39	321	27.3	607	S49528	endoxylinase - rum
40	291	27.3	607	S24754	endo-1,4-beta-xylinase
41	285.5	26.8	608	B51295	xylinase (EC 3.2.1)
42	280	26.3	50	A61149	endo-1,4-beta-xylinase
43	240.5	22.6	266	S48865	endo-1,4-beta-xylinase
44	119	11.2	2817	B97033	uncharacterized pr
45	113.5	10.6	1053	B70987	probable PPE prote

ALIGNMENTS

RESULT 1
S39154
xylinase 1 - fungus (Trichoderma reesei)
C/Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 22-Jun-1999
C/Species: Trichoderma reesei
C/Accession: S39154
R/Toetoeenen, A.; Mach, R.L.; Messner, R.; Gonzalez, R.; Kalkinen, N.; Harkki, A.; Kub
Biotechnology 10, 1461-1465, 1992
A/Title: The two major xylinases from trichoderma reesei: characterization of both enzym
A/Reference number: S39154
A/Accession: S39154
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-222 <TOE>
A/Cross-references: EMBL:X69573; NID:q396563; PIDN:CAA49293.1; PID:q396564
A/Genetics:
A/Gene: xyn1
A/Introns: 90/2
C/Superfamily: endo-1,4-beta-xylinase; endo-1,4-beta-xylinase homology
F:44-222/Domain: endo-1,4-beta-xylinase homology <XYL>

Query Match
Best Local Similarity 95.4%; Score 1017; DB 2; Length 222;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIOPGTGNNGYFYSTYWDHGQVYTNNGPQGFPSVWMSNGNFVGSKGMQPTKXVI 60
DB 33 QTIOPGTGNNGYFYSTYWDHGQVYTNNGPQGFPSVWMSNGNFVGSKGMQPTKXVI 92

QY 61 NFSGSYNPNNGSYLSVYGMSSNPLEYIVENFGYVNSTGATKLGECTCGSVYDIYRT 120
DB 93 NFSGSYNPNNGSYLSVYGMSSNPLEYIVENFGYVNSTGATKLGECTCGSVYDIYRT 152

QY 121 QVNPQSIIGATFYQYVVRNRRSSGSVNTACHFNCMAHGTLTGMDYQIVAVEGYF 180
DB 153 QVNPQSIIGATFYQYVVRNRRSSGSVNTACHFNCMAHGTLTGMDYQIVAVEGYF 212

QY 181 SSGSASITVS 190
DB 213 SSGSASITVS 222

RESULT 2
S39883
endo-1,4-beta-xylinase (EC 3.2.1.8) II precursor - fungus (Trichoderma reesei)
N/Alternate names: endoxylinase II
C/Species: Trichoderma reesei
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C/Accession: S39883; S39884
R/Saarelainen, R.; Paloheimo, M.; Pajetstroem, R.; Suominen, P.L.; Nevalainen, K.M.H.
Mol. Gen. Genet. 241, 497-503, 1993
A/Title: Cloning, sequencing and enhanced expression of the Trichoderma reesei endoxylin

A:Reference number: S39883; MUID:94088442; PMID:8264524
 A:Accession: S39883
 A:Molecule type: DNA
 A:Residues: 1-223 <SAB>
 A:Cross-references: EMBL:567387, NID:9455906; PDB:1AB29346.1; PDB:9455907
 A:Experimental source: strain QM6a
 A:Accession: S39884
 A:Molecule type: protein
 A:Residues: 34-43/49-57/121-151/178-191 <SAF>
 C:Genetics:
 A:Gene: xln2
 A:Introns: 91/2
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylanosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; hydrolyase; polysaccharide degradation
 C:Keywords: glycoprotein; glycosidase; hydrolyase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <PRO>
 F:20-33/Domain: propeptide #status predicted <SIG>
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
 F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:77-94/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:110-121/Binding site: substrate (tyr) #status predicted
 F:119-210/Active site: Glu #status predicted

Query Match 95.4%; Score 1017; DB 2; Length 223;
 Best Local Similarity 97.4%; Pred. No. 2e-72; Indels 0; Gaps 0;
 Matches 185; Conservative 0; Mismatches 5;

QY 1 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 60
 Db 34 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 93

QY 61 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120
 Db 94 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 153

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 180
 Db 154 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 213

QY 181 SSGSASITVS 190
 Db 214 SSGSASITVS 223

RESULT 3
 A44594
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
 N:Alternate names: xylanase IIA
 C:Species: Trichoderma viride
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
 C:Accession: A44594
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44594
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylanosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
 F:112-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:77-88/Binding site: substrate (tyr) #status predicted
 F:86-177/Active site: Glu #status predicted

Query Match 93.2%; Score 994; DB 1; Length 190;
 Best Local Similarity 94.7%; Pred. No. 1.1e-70; Indels 0; Gaps 0;
 Matches 180; Conservative 3; Mismatches 7;

QY 1 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 60

Db 1 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 60

QY 61 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 180
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 180

QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 4
 A44595
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)
 N:Alternate names: xylanase IIB
 C:Species: Trichoderma viride
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
 C:Accession: A44595
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44595
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylanosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolyase; polysaccharide degradation
 F:112-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:86-177/Active site: Glu #status predicted
 F:126-127/Cleavage site: pro-ser (unidentified proteinase) #status predicted
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 92.9%; Score 990; DB 1; Length 190;
 Best Local Similarity 94.2%; Pred. No. 2.2e-70; Indels 0; Gaps 0;
 Matches 179; Conservative 3; Mismatches 8;

QY 1 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 60
 Db 1 QTIQGTGNNNGFYFYSYNNNDHGCVTYTNGPGQFVSVMNSNGNFVGGKMGQPTKXVI 60

QY 61 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120
 Db 61 NFSGSYNPNNGSYLSYVGMSRNPLEYIYVENFGTNPSTGATKLGECTCDGSYYDIYRT 120

QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 180
 Db 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTACHFCMAOHGTLTGMDOYQIVAVEGYF 180

QY 181 SSGSASITVS 190
 Db 181 SSGSASITVS 190

RESULT 5
 A44593
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain
 N:Alternate names: xylanase
 C:Species: Trichoderma harzianum
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
 C:Accession: A44593
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44593
 A:Molecule type: protein

A:Residues: 1-190 <YAG>
 A:Experimental source: strain 358
 R:Campbell, R.L.; Rose, D.R. Protein Data Bank, June 1994
 Submitted to the Brookhaven Protein Data Bank, June 1994
 A:Reference number: A52868; PDB:1XND
 A:Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46; A'48-190
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:86.177/Active site: Glu #status experimental

Query Match 92.0%; Score 981; DB 1; Length 190;
 Best Local Similarity 93.2%; Pred. No. 1,1e-69; Indels 0; Gaps 0;
 Matches 177; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNGYYSYWNDDGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 60
 Db 1 QTIQPGTGYNSGYYSYWNDDGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 60
 QY 61 NFSGSYVPMNSYLSYVGMSPNPLEYIVENFGTTPSPGATKLGECTCDGSYDYIRT 120
 Db 61 NFSGSYVPMNSYLSYVGMSPNPLEYIVENFGTTPSPGATKLGECTCDGSYDYIRT 120
 QY 121 QRVNOPSITGATFYQYWSYRNRHSSGSVNTACHFNCMAQHGILLGTMDYQIVAVEGYF 180
 Db 121 QRVNOPSITGATFYQYWSYRNRHSSGSVNTAHNFAMASHGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASTVS 190
 Db 181 SSGSASTVS 190

RESULT 6
 S71473
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
 C:Species: Chaetomium gracile
 C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C:Accession: S71473; S78207
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asp
 A:Reference number: S71472; MUID:96118924; PMID:8595661
 A:Accession: S71473
 A:Molecule type: DNA
 A:Residues: 1-241 <YOS>
 A:Cross-references: EMBL:D49851; NID:g1339859; PIDD:BA08650.1; PID:g1339860
 A:Accession: S78207
 A:Molecule type: protein
 A:Residues: 38-44;89-91;153-161 <YOH>
 C:Genetics: 88/2
 A:Insertions:
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
 F:43-220/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:116.207/Active site: Glu #status predicted

Query Match 70.9%; Score 755.5; DB 2; Length 241;
 Best Local Similarity 72.7%; Pred. No. 5.7e-52; Indels 1; Gaps 1;
 Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYNNGFYYSYNDGGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 66
 Db 38 TGTNNGFYYSYNDGGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 66
 QY 67 NPMGNSYLSYVGMSPNPLEYIVENFGTTPSPGATKLGECTCDGSYDYIRTQVNOP 126

Db 97 NPMGNSYLSYVGMSPNPLEYIVENFGTTPSPGATKLGECTCDGSYDYIRTQVNOP 156
 QY 127 SIIGTATFYQYWSYRNRHSSGSVNTACHFNCMAQHGILLGTMDYQIVAVEGYSSGSAS 186
 Db 157 SIIGTATFYQYWSYRNRHSSGSVNTACHFNCMAQHGILLGTMDYQIVAVEGYSSGSAT 216
 QY 187 ITV 189
 Db 217 VNV 219

RESULT 7
 S71472
 endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
 N:Alternate names: xylanase A
 C:Species: Chaetomium gracile
 C>Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C:Accession: S71472; S78206
 R:Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A:Title: Two family G xylanase genes from Chaetomium gracile and their expression in As
 A:Reference number: S71472; MUID:96118924; PMID:8595661
 A:Accession: S71472
 A:Molecule type: DNA
 A:Residues: 1-219 <YOS>
 A:Cross-references: EMBL:D49850; NID:g1339857; PIDD:BA08649.1; PID:g1339858
 A:Accession: S78206
 A:Molecule type: protein
 A:Residues: 31-45;82-94;152-160 <YOH>
 C:Genetics: 81/2
 A:Insertions:
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
 F:42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:115.206/Active site: Glu #status predicted

Query Match 65.2%; Score 695.5; DB 2; Length 219;
 Best Local Similarity 67.6%; Pred. No. 2.5e-47; Indels 1; Gaps 1;
 Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTYNNNGFYYSYNDGGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 65
 Db 36 GTYNNNGFYYSYNDGGGVYTYNPGGQFSYVMSNSGNFVGKGMQPTKXKVI 65
 QY 66 YNPMNSYLSYVGMSPNPLEYIVENFGTTPSPGATKLGECTCDGSYDYIRTQVNO 125
 Db 95 FSPQNGYLAITGWTQNPVLYIVESPTGIDPSQSKFTIQQDGSYTIYIAKTRVNO 154
 QY 126 PSIIIGTATFYQYWSYRNRHSSGSVNTACHFNCMAQHGILLGTMDYQIVAVEGYSSGSAS 185
 Db 155 PSIIIGTATFYQYWSYRNRHSSGSVNTACHFNCMAQHGILLGTMDYQIVAVEGYSSGSAT 214
 QY 186 SITVS 190
 Db 215 SITVS 219

RESULT 8
 JC7577
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
 N:Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
 C:Species: Aspergillus oryzae
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C:Accession: JC7577; PC7120
 R:Kimura, T.; Suzuki, H.; Furukashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka, B.
 Biosci. Biotechnol. Biochem. 64, 2734-2738, 2000
 A:Title: Molecular cloning, overexpression, and purification of a major xylanase from As
 A:Reference number: JC7577; MUID: 21077500; PMID:11210150
 A:Accession: JC7577

A:Molecule type: DNA
A:Residues: 1-232 <XIM>
A:Cross-references: DDBJ:AB044941
A:Experimental source: strain KEN616
A:Accession: PC7120
A:Molecule type: protein
A:Residues: 45-64 <K12>
C:Comment: This enzyme has strong similarity to other fungal family 11 endoxylanases, de
C:Genetics:
A:Gene: xymG2
A:Introns: 100/2
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase

Query Match 63.9%; Score 681.5; DB 2; Length 232;
Best Local Similarity 65.6%; Pred. No. 3,3e-46;
Matches 120; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 50 TGYNNGYFYFMTDGGDVTYTNNGSGSYVQWNSVGNFVGGKMGPGS-SRAITYSGSF 108
QY 67 NPNGNSYLSVYGMSNPILIEYIYENFGTYNPGTATKLGECTCDGSVDYRTQRYNP 126
DB 109 NPSGNGYLAIVYGWTTPLIEYIYVESYGTYNPGSGGYTKGQVTSIDGTYNITVSRTNAP 168
QY 127 SIIGTATFYQYWSVRNHRSSGSVNTACHFNCWAQHGLTGTMDYQIIVAVEGFSSGSAS 186
DB 169 SIIGTATFYQFWSVTSKRVGTVTGNHNNAKKGLTGTNTYQIIVAVEGFSSGSAS 228
QY 187 ITV 189
DB 229 ITV 231

RESULT 9
S57477
endo-1,4-beta-xylanase (EC 3.2.1.8) 1 precursor - *Emeticella nidulans*
N:Alternate names: xylanase 1
C:Species: *Emeticella nidulans*, *Aspergillus nidulans*
C>Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 23-Mar-2001
C:Accession: S57477
R:Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes fro
A:Reference number: S57469
A:Accession: S57477
A:Molecule type: DNA
A:Residues: 1-225 <PER>
A:Cross-references: EMBL:Z49892; NID:g870832; PID:CAA90073.1; PID:g870833
C:Genetics:
A:Introns: 93/2
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-225/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
F:121,212/Active site: Glu #status predicted

Query Match 62.0%; Score 660.5; DB 1; Length 225;
Best Local Similarity 63.9%; Pred. No. 1.4e-44;
Matches 117; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 43 TGMNSGYYSFMTDGGCVTTNNGAGSYTVQWNSVGNFVGGKMGPGS-TRITNYGGSF 101
QY 67 NPNGNSYLSVYGMSNPILIEYIYENFGTYNPGTATKLGECTCDGSVDYRTQRYNP 126
DB 102 NPSGNGYLAIVYGWTTPLIEYIYVESYGTYNPGSGGGYRGVTSIDGTYNITVSRTNAP 161

QY 127 SIIGTATFYQYWSVRNHRSSGSVNTACHFNCWAQHGLTGTMDYQIIVAVEGFSSGSAS 186
DB 162 SIIGTATFYQFWSVTSKRVGTVTGNHNNAKKGLTGTNTYQIIVAVEGFSSGSAS 228
QY 187 ITV 189
DB 222 ITV 224

RESULT 10
S57469
endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - *Emeticella nidulans*
N:Alternate names: xylanase 2
C:Species: *Emeticella nidulans*, *Aspergillus nidulans*
C>Date: 10-Oct-1995 #sequence_revision 22-Nov-1996 #text_change 08-May-1998
C:Accession: S57469
R:Perez-Gonzalez, J.A.
submitted to the EMBL Data Library, June 1995
A:Description: Expression in *Saccharomyces cerevisiae* of two xylanase encoding genes fr
A:Reference number: S57469
A:Accession: S57469
A:Molecule type: DNA
A:Residues: 1-221 <PER>
A:Cross-references: EMBL:Z49893; NID:g870834; PID:g870835
C:Genetics:
A:Introns: 89/3
C:Function:
A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xyans
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:19-221/Product: endo-1,4-beta-xylanase 1 #status predicted <MAT>
F:44-221/Domain: endo-1,4-beta-xylanase homology <XYL>
F:117,208/Active site: Glu #status predicted

Query Match 60.9%; Score 649.5; DB 1; Length 221;
Best Local Similarity 64.1%; Pred. No. 9.8e-44;
Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYNNGYFYSYWMDHGCVTTNPGGQFVSVMNSNGNFVGGKMGQPGTKNKVINFSGSY 66
DB 39 TGTSGGYYSFMTDGGDVTYTNNGDGSYVETWTKVGNFVGGKMGPGS-SQTISYGSF 97
QY 67 NPNGNSYLSVYGMSNPILIEYIYENFGTYNPGTATKLGECTCDGSVDYRTQRYNP 126
DB 98 IPSGNGYLSVYGWTTPLIEYIYVESYGTYNPGSGGYTKGQVTSIDGTYNITVSRTNAP 157
QY 127 SIIGTATFYQYWSVRNHRSSGSVNTACHFNCWAQHGLTGTMDYQIIVAVEGFSSGSAS 186
DB 158 SIIGTATFYQFWSVTSKRVGTVTGNHNNAKKGLTGTNTYQIIVAVEGFSSGSAS 217
QY 187 ITVS 190
DB 218 ITVS 221

RESULT 11
UC7307
endo-1,4-beta-xylanase (EC 3.2.1.8) - *Penicillium* sp.
N:Alternate names: Penicillium sp.
C:Species: *Penicillium* sp.
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: UC7307; PC7086
R:Kimura, T.; Ito, J.; Kawano, A.; Makino, T.; Kondo, H.; Karita, S.; Sakka, K.; Ohmiya
Biosci. Biotechnol. Biochem. 64, 1230-1237, 2000
A:Title: Purification, characterization, and molecular cloning of acidophilic xylanase
A:Reference number: UC7307
A:Accession: UC7307
A:Molecule type: DNA
A:Residues: 1-221 <KIM>
A:Cross-references: DDBJ:AB035540

A.Accession: EC7086
A.Molecule type: protein
A.Residues: 32-51 <R12>
C.Genetics:
A.Gene: xyna
A.Introns: 89/2
C.Superfamily: endo-1,4-beta-xylinase, endo-1,4-beta-xylinase homology
C.knowns: glycoprotein, glycosidase, hydrolase

Query Match	59.3%;	Score 632;	DB 2;	Length 221;
Best Local Similarity	59.7%;	Pred. No. 2.3e-42;		
Matches 114;	Conservative 30;	Mismatches 45;	Indels 2;	Gaps 2

QY 60 INFGSSNPNGNSISLSTAYGCMRNPLLEYYIVANFGVNPSTGATPLGCGTCDGSGVYDIYR 119
Db 91 ITFEGTGNPSGNAYLAVYGMTTSPLEYYIILEDYGDYNGNSMTYKGVFTSDGSDYDIYE 150
QY 120 TORNPQESITGTAFTPOYMSVRNHNHSSGSNVTACHENCMQOHGLTGTMYOIVANEGY 179
Db 151 HQCNQNSISGATFNQYMSIRONTSSSTVTITAHFNAMAKLGNLSSFNQIVSTSEGY 210
QY 180 FSSGSASITVS 190
Db 211 ESGGSSTITVS 221

RESULT 12
S43919
endo-1,4-beta-xyylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
C:Species: Humicola insolens
C:Date: 19-Mar-1997 #sequence_rev:slon 19-Mar-1997 #text_change 22-Jun-1999
C:Accession: S43919
R:Dalboge, H.; Heidt-Hansen, H.P.
Mol. Gen. Genet. 243: 253-260, 1994
A:Title: A novel method for efficient expression cloning of fungal enzyme genes.
A:Reference number: S43919; WUID:94247364; PMID:8190078
A:Accession: S43919
A:Molecule type: mRNA
A:Residues: 1-227 <DAL>
A:Cross-references: EMBL:X76047; NID:g505260; PIDD:CAA5632.1; PID:g505261
C:Genetics:
A:Gene: XylI
C:Function:
A:Pathway: xylan degradation
C:Superfamily: endo-1,4-beta-xyylanase; endo-1,4-beta-xyylanase homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-227/Product: endo-1,4-beta-xyylanase #status predicted <MAT>
F:48-225/Domain: endo-1,4-beta-xyylanase homology <XLY>
F:112,123,157/Binding site: substrate (Try, Tyr, Arg) #status predicted
F:121,122/Active site: Glu #status predicted

Query March	56.9%	Score 606.5	DB 2	Length 227
Best Local Similarity	58.2%	Pred. No. 2.3e-40		
Matches 106	Conservative 25	Mismatches 50	Indels 1	Gaps 1
QY	8	GINNGYFYISYANDGHCGVTTYYNGPGGQPSVMSNSGNGFVGKGMQPGTKXKVIINFSGSYN	67	
Db	44	GWINGGYFYSMWSDGGGQVOYTYLTLESGSRQYRWMRNTGNFVGKGMNPGT-CRTINYGYPEN	102	
QY	68	PENNSLSTSYGMSRNPLETEYVVENHFGYVNSPTATLSECTDDSGSYDIYRKORNOQS	127	
Db	103	PQNGGLAYAGWTRNPLVEYVYISYGYINGSGSAQYKGFYTDGQYDILFVSTRNOQS	162	
QY	128	IICTATFYQYSVRANRHSRSGSVNACHFNCAQCHGLTLGTMDYQYIAVAGYSSGSAI	187	
Db	163	IDGTRFPGQYWSIRKNKRQYVSGVNNQNHFNMQOHGMPLOQHYQYVATBGVYSSGSDI	222	
QY	188	TV 189		

Db 223 YV 224

RESULT 13
A44597
endo-1,4-beta-xylanase (EC 3.2.1.8) A - bracket fungus (Schizophyllum commune)
N/Alternate names: xylanase A
C/Species: Schizophyllum commune
C/Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 06-Dec-1996
A/Accession: A44597; S41411; A05147; S38973
R/Yaguchi, M.
submitted to the Protein Sequence Database, March 1994
A/Reference number: A44593

[illegible]

N/Alternate names: xylanase B
 C/Species: Streptomyces lividans
 C/Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
 C/Accession: J050590; F50239
 R/Shareck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
 Gene 107, 75-82, 1991
 A/Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
 A/Reference number: J050591; MIMD:92077439; PMID:1143521
 A/Accession: U050590
 A/Molecule type: DNA
 A/Residues: 1-333 <SHA>
 A/Cross-references: GB:M64552
 A/Accession: P80239
 A/Molecule type: protein
 A/Residues: 41-71 <SH2>
 C/Genetics:
 A/Gene: xlnB
 C/Function:
 A/Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A/Pathway: xylan degradation
 C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
 C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F/1-40/Domain: signal sequence #status predicted <SIG>
 F/41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
 F/54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
 F/127,217/Active site: Glu #status predicted

Query Match 53.2%; Score 567; DB 1; Length 333;
 Best Local Similarity 52.5%; Pred. No. 4.2e-37;
 Matches 104; Conservative 33; Mismatches 45; Indels 16; Gaps 5;

```

QY 5 PGT-----GYNNGYFYSYMNDSHGAVTYTNGPGGQFSPVWMSNGNFVGGKQW 52
Db 35 PGTADPTVTTNDEGTNGGYYSFWTDSQGTVMNMGSGQYSTSRNTGNFVAGKGM 94
QY 53 PGTAKXINFSGSINPENGSTLSVYGSRRPPLIEYIVENFGTYNPSGTATKLGECTCDG 112
Db 95 NGGR-RTVQYSGSNFSGNAYLALYGMTSNPLVEYIVDWNGYTRP-TGEYK-GTYTSDG 151
QY 113 SVYDIYRTQRYNCPISIIIGTATFYQYWSVRNRHSSGSVNTACHFNCWAQGLTLGTWD-Y 171
Db 152 GTYDIYKTRNKRPSVSGTRTFDQYWSVRQAKRTGTITGNHFDAMARAGMPLGNFSY 211
QY 172 QIVAVEGYFSSGSASTV 189
Db 212 MIMATEGYSSGSSSINV 229

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RESULT 15

T50601
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
 N/Alternate names: xylanase B
 C/Species: Streptomyces coelicolor
 C/Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
 C/Accession: T50601
 R/Redenbach, M.; Kleser, H.M.; Denapalte, D.; Richner, A.; Cullum, J.; Kinashi, H.; Hopy
 M.O. Microbiol. 21, 77-96, 1996
 A/Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb S
 A/Reference number: Z20556; MIMD:97000351; PMID:8843436
 A/Accession: T50601
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-335 <RED>
 A/Cross-references: EMBL:AL133320; PIDN:CAB61738.1
 A/Experimental source: strain AS(2)
 C/Genetics:
 A/Gene: xlnB
 C/Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
 C/Keywords: glycosidase; hydrolase

Query Match 53.2%; Score 567; DB 2; Length 335;
 Best Local Similarity 53.0%; Pred. No. 4.2e-37;
 Matches 105; Conservative 31; Mismatches 46; Indels 16; Gaps 5;

```

QY 5 PGT-----GYNNGYFYSYMNDSHGAVTYTNGPGGQFSPVWMSNGNFVGGKQW 52
Db 36 PGTADPTVTTNDEGTNGGYYSFWTDSQGTVMNMGSGQYSTSRNTGNFVAGKGM 95
QY 53 PGTAKXINFSGSINPENGSTLSVYGSRRPPLIEYIVENFGTYNPSGTATKLGECTCDG 112
Db 96 NGGR-RTVQYSGSNFSGNAYLALYGMTSNPLVEYIVDWNGYTRP-TGEYK-GTYTSDG 152
QY 113 SVYDIYRTQRYNCPISIIIGTATFYQYWSVRNRHSSGSVNTACHFNCWAQGLTLGTWD-Y 171
Db 153 GTYDIYKTRNKRPSVSGTRTFDQYWSVRQAKRTGTITGNHFDAMARAGMPLGNFSY 212
QY 172 QIVAVEGYFSSGSASTV 189
Db 213 MIMATEGYSSGSSSINV 230

```

Search completed: June 30, 2004, 19:41:14
 Job time : 14 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 Seconds
(without alignments)
1364.597 Million cell updates/sec

Title: US-09-856-025b-64

Perfect score: 1066
Sequence: 1 QTIQPGTGNNGYFYSYND.....YQIIVAEVGFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141661 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	95.4	222	1 XYN2_TRIRE	P36217 trichoderma
2	975	91.5	190	1 XYN1_TRIHA	P48793 trichoderma
3	660.5	62.0	225	1 XYN1_EMENTI	P55332 emericella
4	652.5	61.2	225	1 XYN2_ASPEKA	P48862 aspergillus
5	649.5	60.9	221	1 XYN2_EMENTI	P55323 emericella
6	647.5	60.7	225	1 XYN1_THELA	O43097 thermomyces
7	640.5	60.1	225	1 XYN2_ASPEKA	P55330 aspergillus
8	633.5	59.4	221	1 XYN1_COCCA	O06562 cochliobola
9	606.5	56.9	227	1 XYN1_HUMIN	P55334 humicola
10	577.5	54.2	197	1 XYN1_SCHCO	P35809 schizopyll
11	570	53.5	335	1 XYN2_STRLI	P26515 streptomyces
12	559.5	52.5	233	1 XYN2_MAGRA	P55325 magnaporthe
13	550.5	51.6	644	1 XYN2_CELFI	P54865 cellulomona
14	503	47.2	240	1 XYN1_STRLI	P26220 streptomyces
15	500.5	47.0	210	1 XYN1_BACST	P45705 bacillus st
16	488	45.8	213	1 XYN1_BACSU	P18429 bacillus su
17	487	45.7	213	1 XYN1_BACCI	P09850 bacillus ci
18	458	43.0	228	1 XYN1_BACPU	P00694 bacillus pu
19	441.5	41.4	261	1 XYN1_CLOSA	P17137 clostridium
20	430	40.3	512	1 XYN1_CLOSR	P33358 clostridium
21	419	39.3	211	1 XYN1_ASPEKA	P55338 aspergillus
22	419	39.3	211	1 XYN1_ASPEKA	P55339 aspergillus
23	418.5	39.3	229	1 XYN1_TRIRE	P36218 trichoderma
24	417	39.1	211	1 XYN1_ASPTU	P55331 aspergillus
25	414	38.8	211	1 XYN3_ASPEKA	P33567 aspergillus
26	388	36.4	954	1 XYN1_RUMFL	P29126 ruminococcu
27	375.5	35.2	802	1 XYN2_RUMFL	O53317 ruminococcu
28	360.5	33.8	179	1 XYN1_PSEXY	P83513 pseudobuty
29	291	26.8	607	1 XYN1_NEOPA	P29127 neocallima
30	285.5	26.0	608	1 XYN1_FIBSU	P35811 fibrobacter
31	245	23.0	625	1 XYN1_FIRSP	O12667 pithomyces s
32	100.5	9.4	159	1 GRPA_MEDPA	O09134 medicago fa
33	100	9.4	513	1 GUX1_TRIVI	P19355 trichoderma

ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD:	PRT:	222 AA.	
AC	P36217					P52090 pseudomonas
DT	01-JUN-1994 (Rel. 29, Created)					P00725 trichoderma
DT	01-JUN-1994 (Rel. 29, Last sequence update)					P41640 pinus thunb
DT	28-FEB-2003 (Rel. 41, Last annotation update)					O856X0 pinus korai
DE	Endo-1,4-beta-xylanase 2 precursor (Ec 3.2.1.8) (Xylanase 2)					P58386 triticum ae
DE	(1,4-beta-D-xylan xylanhydrolase 2).					P04967 zea mays (m
GN	XYN2.					O91YV5 neisseria m
OS	Trichoderma reesei (Hypocrea jecorina).					P51990 xenopus lae
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;					P12256 oryza sativ
OX	Hypocreales; Hypocreales; Hypocreales; Hypocrea.					O88569 mus musculu
OX	NCBI_TaxID=51453;					O00548 cryphonectr
RN	(1)					
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
RC	STRAIN=C30;					
RX	MEDLINE=93103679; PubMed=1369024;					
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,					
RT	Harkki A., Kudrick C.P.,					
RT	"the two major xylanases from Trichoderma reesei: characterization of					
RL	both enzymes and genes."					
RL	Biotechnology 10:1461-1465(1992).					
RL	(2)					
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).					
RC	STRAIN=C30;					
RX	MEDLINE=94283373; PubMed=8013449;					
RA	Toerrien A., Harkki A., Rouvinen J.;					
RT	Three-dimensional structure of endo-1,4-beta-xylanase II from					
RT	Trichoderma reesei: two conformational states in the active site."					
RL	EMBO J. 13:2493-2501(1994).					
RN	(3)					
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).					
RC	STRAIN=C30;					
RX	MEDLINE=95127663; PubMed=7827044;					
RA	Toerrien A., Rouvinen J.;					
RT	"Structural comparison of two major endo-1,4-xylanases from					
RT	Trichoderma reesei."					
RL	Biochemistry 34:847-856(1995).					
RN	(4)					
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).					
RC	STRAIN=C30;					
RX	MEDLINE=96502263; PubMed=8755744;					
RA	Havukainen R., Toerrien A., Laitinen T., Rouvinen J.;					
RT	"Covalent binding of three epoxalyxyl xylosides to the active site of					
RT	endo-1,4-xylanase II from Trichoderma reesei."					
RL	Biochemistry 35:9617-9624(1996).					
CC	-1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xylosidic					
CC	linages in xylans.					
CC	-1- PATHWAY: Xylan degradation.					
CC	-1- PTM: The N-terminus is blocked.					
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl					
CC	hydrolases).					
CC	-----					
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DR EMBL; X69573; CAA49293.1; .
DR PIR; S39154; S39154.
DR PDB; 1XVO; 08-AUG-95.
DR PDB; 1XVP; 08-AUG-95.
DR PDB; 1ENX; 08-AUG-95.
DR PDB; 1RED; 11-JAN-97.
DR PDB; 1REF; 11-JAN-97.
DR InterPro; IPR008985; Cona_like_1ec_g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE1.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
KW 3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 222
FT ACT_SITE 118 118
FT ACT_SITE 209 209
FT CARBOHYD 70 70
FT CARBOHYD 93 93
FT CARBOHYD 129 129
FT STRAND 34 35
FT TURN 38 42
FT TURN 43 44
FT STRAND 45 51
FT STRAND 57 61
FT TURN 64 65
FT STRAND 66 71
FT STRAND 76 83
FT STRAND 91 101
FT STRAND 104 113
FT STRAND 114 116
FT TURN 117 125
FT TURN 130 133
FT STRAND 135 142
FT TURN 143 144
FT STRAND 145 157
FT TURN 160 161
FT STRAND 164 173
FT STRAND 180 183
FT HELIX 184 193
FT TURN 194 195
FT STRAND 200 211
FT STRAND 214 222
SQ SEQUENCE 222 AA; 24172 MM; 15F7032FACF963FF CRC64;

Query Match 95.4%; Score 1017; DB 1; Length 222;
Best Local Similarity 97.4%; Pred. No. 8.2e-79;
Matches 185; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 QTIQPGGNGNGYFYSWNDHGGVYTNNGGCGFSVWMSNGNFVGGKMGPGTKXKVI 60
DB 33 QTIQPGGNGNGYFYSWNDHGGVYTNNGGCGFSVWMSNGNFVGGKMGPGTKXKVI 92
OY 61 NFSGSYNNGNSYFVYSGWNRNPLIEYIYENFTYPSGATLGGCTDDGSYVDIYRT 120
DB 93 NFSGSYNNGNSYFVYSGWNRNPLIEYIYENFTYPSGATLGGCTDDGSYVDIYRT 152
OY 121 QRVNOPSITGATFYQWVSVRNRSSGSVNTACHFNCMAQHGTLGTMDYQIYAEGYF 180
DB 153 QRVNOPSITGATFYQWVSVRNRSSGSVNTACHFNCMAQHGTLGTMDYQIYAEGYF 212
OY 181 SSGSASITVS 190
DB 213 SSGSASITVS 222

RESULT 2

ID XYN TRIHA STANDARD; PRT; 190 AA.

AC P46793;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan

DE xylanohydrolase);

OS Trichoderma harzianum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Hypocremetaceae; Hypocreales; Hypocreaceae; Hypocrea.

OX NCBI_TaxID=5544;

RN (1)

RP SEQUENCE.

RC STRAIN=E58;

RA Yaguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,

RA Sadtler J.N.,

RT "The amino acid sequence of the 20 Kd xylanase from Trichoderma

RT harzianum E58."

RL (In) Visser J., Beldman G., Kusters-van Someren M.A.,

RL Voragen A.G., (eds.);

RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).

RM [2]

RA X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).

RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,

RA Yaguchi M.;

RT "High-resolution structures of xylanases from B. glaucans and

RT T. harzianum identify a new folding pattern and implications for the

RT atomic basis of the catalysis."

RL (In) Suominen P., Reinikainen T. (eds.);

RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,

RL Foundation for Biotechnical and Industrial Fermentation Research,

RL Helsinki (1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic

CC linkages in xylans.

CC -1- PATHWAY: Xylan degradation.

CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

CC hydrolases).

DR PDB; 1XND; 20-DEC-94.

DR InterPro; IPR008985; Cona_like_1ec_g1.

DR InterPro; IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GLHYDRLASE1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.

FT ACT_SITE 86 86

FT ACT_SITE 177 177

FT ACT_SITE 177 177

FT STRAND 3 3

FT STRAND 6 9

FT STRAND 14 19

FT STRAND 25 29

FT TURN 32 33

FT STRAND 34 39

FT TURN 44 51

FT TURN 56 57

FT STRAND 59 69

FT STRAND 72 81

FT TURN 82 84

FT STRAND 85 93

FT TURN 98 101

FT STRAND 103 110

FT TURN 111 112

FT STRAND 113 125

FT TURN 128 129

FT STRAND 132 141

FT STRAND 148 151

FT HELIX 152 161

FT TURN 162 163

FT STRAND 168 179

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FT STRAND 182 190
SQ SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;

Query Match
Best Local Similarity 91.5%; Score 975; DB 1; Length 190;
Matches 176; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 QTIOPGCGYNNNGYRYSYVNDGCGVTTTNGPGGQFVSVMNSGNGFVGAKGMPGTRKRV 60
DB 1 QTIOPGCGYNNNGYRYSYVNDGCGVTTTNGPGGQFVSVMNSGNGFVGAKGMPGTRKRV 60
QY 61 NFSGNSYVNGSYLVGMSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSYVDIYRT 120
DB 61 NFSGNSYVNGSYLVGMSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSYVDIYRT 120
QY 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGLTLGTMVQIYVAEGYF 180
DB 121 QRVNQPSTIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGLTLGTMVQIYVAEGYF 180
QY 161 SSGSASITVS 190
DB 161 SSGSASITVS 190
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XYN1 EMENT
ID XYN1 EMENT STANDARD; PRT; 225 AA.
AC P55353; Q00173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
OS Emeritella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emeritella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236210; PubMed=8787417.
RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
RT Aspergillus nidulans xylanase genes."
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z49892; CA90073.1;
CC PIR; S57477; S57477.
CC HSSP; P48793; 1XND.
CC InterPro; IPR008985; ConA_like_1ec.g1.
CC InterPro; IPR01137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11.
CC PRINTS; PR00911; GLYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; signal.
FT SIGNAL 1
FT CHAIN 19
FT ACT_SITE 121 225
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRC64;

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Query Match
Best Local Similarity 62.0%; Score 660.5; DB 1; Length 225;
Matches 117; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGVNNGYFYFSYVNDGCGVTTTNGPGGQFVSVMNSGNGFVGAKGMPGTRKRV 66
DB 43 TGVNNGYFYFSYVNDGCGVTTTNGPGGQFVSVMNSGNGFVGAKGMPGTRKRV 66
QY 67 NFSGNSYLVGMSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSYVDIYRTORVNP 126
DB 102 NFSGNSYLVGMSRNPLEYIYVENFGTYNPSTGATKLGECTCDGSYVDIYRTORVNP 126
QY 127 SIIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGLTLGTMVQIYVAEGYFSSGSAS 186
DB 162 SIIGTATFYQVWSVRNRHSSGSVNTACHFNCMAQHGLTLGTMVQIYVAEGYFSSGSAS 221
QY 187 ITV 169
DB 222 ITV 224

RESULT 4
XYNB ASPKA
ID XYNB ASPKA STANDARD; PRT; 225 AA.
AC P48874;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
GN XYNB.
OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=40384;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IFO 4308;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolase of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D38070; BAA0764.1;
CC HSSP; P36217; 1XYO.
CC InterPro; IPR008985; ConA_like_1ec.g1.
CC InterPro; IPR01137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11.
CC PRINTS; PR00911; GLYDRLASE11.
CC PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC Xylan degradation; Hydrolase; Glycosidase; signal.
FT SIGNAL 1
FT CHAIN 19
FT ACT_SITE 121 225
FT ACT_SITE 212 212
SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match
Best Local Similarity 61.2%; Score 652.5; DB 1; Length 225;
Matches 117; Conservative 23; Mismatches 42; Indels 1; Gaps 1;

```

QY 7 TGVNNGYFVSVMNDGCGVYTTNGPGGQFVSVMNSGNFVYGGKQPGTKNKVINSQSY 66
 DB 43 TGVNNGYFVSVMNDGCGVYTTNGNAGSYFVSVMNSGNFVYGGKQPGTKNKVINSQSY 101
 QY 67 NPNNGSYLVSVMGSRNPLIEYIYVENFGTNPSTGATKLGECTDCGSVYDIYRTQVNOP 126
 DB 102 TPGNGYLSYGVMTTDLPIEYIYVESYGVNPGSGGTRGNVSSDGSVYDIYATRTNAP 161
 QY 127 SIIGTATFYQWYSVRNRHRSQSVNTACHFCNCAOHLTGTMDCYQVAIVEGFSSGSAS 186
 DB 162 SIIGTATFYQWYSVRNRHRSQSVNTACHFCNCAOHLTGTMDCYQVAIVEGFSSGSAS 221
 QY 187 ITVS 189
 DB 222 ITI 224

RESULT 5

XYN2 EMENI STANDARD; PRT; 221 AA.
 ID XYN2 EMENI
 AC P5533; 000176;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
 DE (1,4-beta-D-xylan xylanohydrolase 2).
 OS Emericella nidulans (Aspergillus nidulans).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; Emericella.
 CX NCBI_TaxID=162425;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96236210; PubMed=8787417;
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;
 RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two
 RT *Aspergillus nidulans* xylanase genes.";
 RL Appl. Environ. Microbiol. 62:2179-2182 (1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL; 249893; CA90074.1; -;
 DR PIR; S57469; S57469.
 DR HSSP; P48793; IXND.
 DR InterPro; IPR008985; Cons. like lec_g1.
 DR InterPro; IPR001337; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11.1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1
 FT CHAIN 19
 FT ACT_SITE 117
 FT ACT_SITE 208
 SQ SEQUENCE 221 AA; 23517 MW; 4266EB9DDDB9475 CRC64;

Query Match 60.9%; Score 649.5; DB 1; Length 221;
 Best Local Similarity 64.1%; Pred. No. 7.1e-48;
 Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

DB 39 TGTSGYYYSFWTDGGADVYTTNDGGSYFVEMTKVNFVGGKQPNFS-SQITISYGSF 97
 QY 67 NPNNGSYLVSVMGSRNPLIEYIYVENFGTNPSTGATKLGECTDCGSVYDIYRTQVNOP 126
 DB 98 IPSNGYLSYGVMTTDLPIEYIYVESYGVNPGSGGTRGNVSSDGSVYDIYATRTNAP 157
 QY 127 SIIGTATFYQWYSVRNRHRSQSVNTACHFCNCAOHLTGTMDCYQVAIVEGFSSGSAS 186
 DB 158 SIIGTATFYQWYSVRNRHRSQSVNTACHFCNCAOHLTGTMDCYQVAIVEGFSSGSAS 217
 QY 187 ITVS 190
 DB 218 ITVS 221

RESULT 6

XYNA THELA STANDARD; PRT; 225 AA.
 ID XYN2 EMENI
 AC P5533; 000176;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Xylanase) (1,4-beta-D-
 DE xylan xylanohydrolase).
 CN XYN2.
 OS Thermomyces lanuginosus (Humicola lanuginosa).
 CC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
 CX NCBI_TaxID=5541;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 5826 / Tsiklinsky;
 RX MEDLINE=97033440; PubMed=8879171;
 RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
 RT "Cloning and characterization of the gene for the thermostable
 RT xylanase Xyna from *Thermomyces lanuginosus*.";
 RL J. Biotechnol. 49:211-218 (1996).
 RN (2)
 RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
 RC STRAIN=DSM 5826 / Tsiklinsky;
 RX MEDLINE=98426042; PubMed=9753433;
 RA Gruber K., Kintner G., Hayn M., Schlacher A., Steiner W.,
 RA Kracky C.;
 RT "Thermophilic xylanase from *Thermomyces lanuginosus*: high-resolution
 RT X-ray structure and modeling studies.";
 RL Biochemistry 37:13475-13485 (1998).
 CC -1- FUNCTION: THERMOSTABLE XYLANASE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL; U35436; AAB94633.1; -;
 DR PDB; 1YNA; 12-FEB-97.
 DR InterPro; IPR008985; Cons. like lec_g1.
 DR InterPro; IPR001337; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11.1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_2; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal; 3D-structure;
 KW Pyriolidone carboxylic acid.
 FT SIGNAL 1
 FT CHAIN 32
 FT END-1,4-BETA-XYLANASE.


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RL Physiol. Mol. plant Pathol. 40:39-47 (1992).
CC - FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
CC WALLS.
CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC - PATHWAY: Xylan degradation.
CC - SUBCELLULAR LOCATION: Secreted.
CC - PFM: The N-terminus is blocked.
CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL: L13596; AAA33024.1; -.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 30
FT CHAIN 31 221
FT ACT_SITE 115 115 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 206 206 PROTON DONOR (BY SIMILARITY).
FT CONFLICT 81 81 W -> I (IN REF. 2).
FT CONFLICT 107 107 G -> A (IN REF. 2).
FT CONFLICT 131 131 S -> W (IN REF. 2).
SQ SEQUENCE 221 AA; 23728 MW; 59D8D983FCSB08C CRC64;

Query Match 59.4%; Score 633.5; DB 1; Length 221;
Best Local Similarity 60.5%; Pred. No. 1.6e-46;
Matches 115; Conservative 25; Mismatches 49; Indels 1; Gaps 1;

QY 1 OTTPGGYNNNGYYSVNDGCGVYTNNGCGQFVSVMNSGNGFVGKGMOPGTRKXVI 60
DB 31 QNTNGAGCTHNGCFWMSWSDGAGARATYTNAGSGYSVMSGGLVGGKMMNGTA-RTI 89
QY 61 NFGSGYNNNGSYLSYVWGSRNPLIEYIVENFGTYNPSGTATKLGCTCDGSEYDIYRT 120
DB 90 TYSGTYYNNGSYLAAYGWTFRNPLVEYVVENFGTYDPSGOSQKGTVTSDGSSYKLAQS 149
QY 121 QNVNOPSITGATYQVWVSVRNRHSSGSVNTACHFNCAQHGTLGTMDYQIVAVEGYF 180
DB 150 TRITNPSIDGTFRITQQTWVSVRNQNRSSGSVNMKTHFAMASKGNLQGHYQIVATBGIY 209
QY 181 SSGASATVS 190
DB 210 STGNAGITVN 219

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RP SEQUENCE FROM N.A.
RX MEDLINE=94247364; PubMed=8190078;
RA Dalboese H., Hansen H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes."
RL Mol. Gen. Genet. 243:253-260 (1994).
CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC - PATHWAY: Xylan degradation.
CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC -----
DR EMBL: X76047; CAA53632.1; -.
DR PIR: S43919; S43919.
DR HSSP: O43097; 1YNA.
DR InterPro: IPR008985; Cons. like lec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 19
FT CHAIN 20 227
FT ACT_SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 227 AA; 25601 MW; 5C2F6ADEFDA1F CRC64;

Query Match 56.9%; Score 606.5; DB 1; Length 227;
Best Local Similarity 58.2%; Pred. No. 3.1e-44;
Matches 106; Conservative 25; Mismatches 50; Indels 1; Gaps 1;

QY 8 GYNNGYFFSYNNNDGCGVYTNNGCGQFVSVMNSGNGFVGKGMOPGTRKXVI 67
DB 44 GHNHNYFFSYNWSDDGGQVQYTNLBSSRYQVRKRTGNGFVGKMMNPT-GRTIVYGGVFN 102
QY 68 PNGNSYLSVWGSRNPLIEYIVENFGTYNPSGTATKLGCTCDGSEYDIYRTORVNOP 127
DB 103 PGNGYLAAYGWTFRNPLVEYVVENFGTYNFGSQAYGTFYTDGDYDIFVSTRYNOPS 162
QY 128 ITGATFPQVWVSVRNRHSSGSVNTACHFNCAQHGTLGTMDYQIVAVEGYFSSGASI 187
DB 163 IDGTRTFQOYVSIKRNKSVGSGVNMQNHFNAMQHGMLGQHYIQVAVATBSYQSSGSIDI 222
QY 188 TV 189
DB 223 YV 224

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RESULT 10
ID XYNX SCHCO STANDARD; PRT; 197 AA.
AC P35809;
DT 01-UTN-1994 (Rel. 29, Created)
DT 01-UTN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
DE xylanohydrolase A).
CN XYNX
OS Schizophyllum commune (Bracket fungus).
OS Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllum.
OC NCBI_TaxID=5334;
RN [1]
RP SEQUENCE.

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RC STRAIN-ATCC 38548 / Delmar;
 RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.,
 RL (in) Vissers J., Beldman G., Kusters-van Someren M.A.,
 RL Voraagen A.G.J. (eds.);
 RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
 RN [2]
 RP SEQUENCE AND DISULFIDE BONDS.
 RC STRAIN-ATCC 38548 / Delmar;
 RX MEDLINE=94063044; PubMed=824336;
 RA Oka T., Roy C., Watson D.C., Wakarchuk W., Campbell R., Yaguchi M.,
 RA Yurasek L., Paice M.G.;
 RT "Amino acid sequence and thermostability of xylanase A from
 RT Schizophyllum commune";
 RL FEBS Lett. 334:296-300(1993).
 RN [3]
 RP PARTIAL SEQUENCE AND ACTIVE SITE GLU-87.
 RC STRAIN-ATCC 38548 / Delmar;
 RX MEDLINE=94155888; PubMed=7906649;
 RA Bray M.R., Clarke A.J.;
 RT "Identification of a glutamate residue at the active site of xylanase
 RT A from Schizophyllum commune";
 RL Eur. J. Biochem. 219:821-827(1994).
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
 CC xylanase has a very broad pH activity.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 DR PIR; A44597; A44597.
 DR HSSP; O43097; IYNA.
 DR InterPro: IPR008985; Cons. like lec gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 KW Xylan degradation; Hydrolase; Glycosidase.
 FT ACT_SITE 87
 FT ACT_SITE 184
 FT DISULFID 111 160 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 197 AA; 20978 MW; 42C8074B67C1FB59 CRC64;
 Query Match 54.2%; Score 577.5; DB 1; Length 197;
 Best Local Similarity 55.0%; Pred. No. 7,3e-42;
 Matches 105; Conservative 34; Mismatches 45; Indels 7; Gaps 3;

DE (1,4-beta-D-xylan xylanohydrolase B).
 GN XLNB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomyces; Streptomyces.
 OC NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.
 RC STRAIN=66 / 1326;
 RX MEDLINE=92077439; PubMed=1743521;
 RA Sharack F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
 RT "Sequences of three genes specifying xylanases in Streptomyces
 RT lividans";
 RL Gene 107:75-82(1991).
 RN [2]
 RP REVISIONS TO 29-32 AND 252-307.
 RC STRAIN=66 / 1326;
 RX MEDLINE=95189090; PubMed=7533741;
 RA Sharack F., Biely P., Morosoli R., Kluepfel D.;
 RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
 RT reveals genes encoding acetyl xylan esterase and the RNA component of
 RT ribonuclease P";
 RL Gene 153:105-109(1995).
 RN [3]
 RP REVISION TO 225.
 RA Sharack F.;
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
 CC component of plant cell-walls. XLNA and XLNB seem to act
 CC sequentially on the substrate to yield xylobiose and xylose
 CC as carbon sources.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
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 CC -----
 DR EMBL; M64552; AAC06114.2; -.
 DR HSSP; P09850; XLNB.
 DR InterPro: IPR001919; Bac_celose-bind.
 DR InterPro: IPR008985; Cellul bind.
 DR InterPro: IPR008985; Cons. like lec gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR SMART; SM00637; CBD_11; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 41
 FT CHAIN 42 335 ENDO-1,4-BETA-XYLANASE B.
 FT DOMAIN 42 230
 FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 250 335 XYLAN-BINDING (POTENTIAL).
 FT ACT_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 335 AA; 35575 MW; 513B1458BF8FC0C CRC64;
 Query Match 53.5%; Score 570; DB 1; Length 335;
 Best Local Similarity 53.0%; Pred. No. 5.6e-41;
 Matches 105; Conservative 32; Mismatches 45; Indels 16; Gaps 5;

Db 36 PGTAQADVTYTTNOEGTNNNGYYSFWTDSQGTIVSNMNGSGQYSTSWRTNGTFVAGKWA 95
 QY 53 PGTRKAKINSSGYNPNKNSYLSTVGMSPNLEIYIVENFGTYNSTGATKLGECTCG 112
 Db 96 NGR-FVQVSGSFNBSGNALYLGYWTSNPLVEYIVDWGTYR-TEBYK-GVYTSIG 152
 QY 113 SYVDIYRTORNOPSIIIGTATFYQYWSVRNHRSSGVNACHFNQWAGHGLTGM-D-Y 171
 Db 153 GTDIYKTTKTVNKPSEVGTTFQYVNSVRSKRTGTTGNHFDAMAPAGMPLGNFSY 212
 QY 172 QIVAVEGFSSGSASTV 189
 Db 213 MIMATEGYSSGSSINV 230

RESULT 12

XYN2_MAGR STANDARD; PRT; 233 AA.
 ID XYN2_MAGR
 AC P55335; Q01171;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
 GN (1,4-beta-D-xylan xylanohydrolase 22).
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.
 CX NCBI_TaxID=148305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K60-19;
 RA MEDLINE=96172742; PubMed=8599407;
 RA Wu S.C., Kautman S., Darvill A.G., Albersheim P.;
 RT "Purification, cloning and characterization of two xylanases from
 RT Magnaporthe grisea, the rice blast fungus.";
 RL Mol. Plant Microbe Interact. 8:506-514(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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CC EMBL; L37529; AAC1683.1; -.
 DR HSSP; O43097; INMA.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDR1AS11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 KW SIGNAL
 FT CHAIN 1 39 POTENTIAL.
 FT ACT SITE 40 233 ENDO-1,4-BETA-XYLANASE 22.
 FT ACT SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 217 217 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;

Query Match 52.5%; Score 559.5; DB 1; Length 233;
 Best Local Similarity 51.3%; Pred. No. 2.9e-40;
 Matches 98; Conservative 33; Mismatches 57; Indels 3; Gaps 2;

QY 1 OTIOGTGNGNGYFYSYNDGAGVYTYNGGCGFVSWSNNGFVGKGMQPGTKXVI 60
 Db 40 OSTPSTGRHNGYYSWTDDGSPVOYQNGNGSGSYVMQSGGNFVGKGMPE-GSKSI 98

QY 61 NFSGSYNP--NGNSYLSVGMSPNLEIYIVENFGTYNSTGATKLGECTCGSYVDIY 118
 Db 99 TYSGTFPVNNGNAYLCIYGTQNPLEVEYILEYNGSYNPNNSQSGTLOAAGTYTLH 158
 QY 119 RTQVNOPSIIIGTATFYQYWSVRNHRSSGVNACHFNQWAGHGLTGM-D-QIVAVEG 178
 Db 159 ESTRNOSTLEGTFPOQYMAIRQOKNSGVNTGTFQAWERAGMGMNMTIVATEG 218
 QY 179 YFSSGSASTV 189
 Db 219 YRSAGSNINV 229

RESULT 13

XYND_CELFI STANDARD; PRT; 644 AA.
 ID XYND_CELFI
 AC P54865;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
 GN XYND..
 OS Cellulomonas fimi.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococciaceae; Cellulomonadaceae; Cellulomonas.
 CX NCBI_TaxID=1708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=221;
 RA MEDLINE=94224155; PubMed=8170399;
 RA Milward-Sadler S.J., Poole D.M., Henriessat B., Hazlewood G.P.,
 RA Clarke J.H., Gilbert H.J.;
 RT "Evidence for a general role for high-affinity non-catalytic
 RT cellulose binding domains in microbial plant cell wall hydrolases.";
 RL Mol. Microbiol. 11:375-382(1994).
 CC -1- FUNCTION: Endo-acting xylanase which displays no detectable
 CC activity against polysaccharides other than xylan. Hydrolyses
 CC glucosidic bonds with retention of anomeric configuration.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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CC EMBL; X76729; CAA54145.1; -.
 DR PIR; I40712; I40712.
 DR PDB; 1ESB; 25-MAY-01.
 DR PDB; 1ESC; 25-MAY-01.
 DR PDB; 1HEH; 10-MAY-01.
 DR PDB; 1HEJ; 10-MAY-01.
 DR PDB; 1XBD; 21-JUL-99.
 DR PDB; 2XBD; 21-JUL-99.
 DR InterPro; IPR001919; Bac_cellose-bind.
 DR InterPro; IPR008985; Cellul_bind.
 DR InterPro; IPR008985; Cona_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR InterPro; IPR002509; Polysac_deacet.
 DR Pfam; PF00553; CBM_2; 2.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR Pfam; PF01522; Polysac_deacet; 1.
 DR PRINTS; PR00911; GLHYDR1AS11.
 DR SMART; SM00637; CBD_11; 2.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KM Xylan degradation; Hydrolyase; Glycosidase; Signal; Repeat;
 3D-structure.
 FT SIGNAL 1 43 POTENTIAL.
 FT CHAIN 44 644 ENDO-1,4-BETA-XYLANASE D.
 FT DOMAIN 44 230 CATALYTIC.
 FT DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 246 644 2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.
 FT REPEAT 246 333 1.
 FT REPEAT 246 333 2.
 FT REPEAT 337 644 LINKER ("HINGE") (PRO-THR BOX).
 FT DOMAIN 348 556 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 231 238 POLY-GLY.
 FT DOMAIN 241 245 POLY-GLY.
 FT DOMAIN 548 558 POLY-GLY.
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 644 AA; 66581 MW; 55B045CC6E0E1820 CRC64;

Query Match 51.6%; Score 550.5; DB 1; Length 644;
 Best Local Similarity 53.5%; Pred. No. 5e-39;
 Matches 99; Conservative 38; Mismatches 43; Indels 5; Gaps 4;

QY 7 TGNNGYFYVYVNDGSGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 66
 DB 49 TGNNGYFYVYVNDGSGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 106

QY 67 NPNNGSYLVYVGSRNPLIEYIVENFGYVNPSTGATKLGECTCDGSGVDYITQRYNOP 126
 DB 107 NPNNGSYLVYVGSRNPLIEYIVENFGYVNPSTGATKLGECTCDGSGVDYITQRYNOP 144

QY 127 SIIG-TATFYQVYVRNHRSSGSVNTACHPCNAGCLTLGTMVDYIVAVEGYPSSGSA 185
 DB 165 SIIG-TATFYQVYVRNHRSSGSVNTACHPCNAGCLTLGTMVDYIVAVEGYPSSGSA 224

QY 186 SITVS 190
 DB 225 SITVS 229

RESULT 14
 XYNL STRLI STANDARD; PRT; 240 AA.
 AC P26220;
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
 DE (1,4-beta-D-xylan xylanohydrolyase C).
 GN XYNL.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
 RC STRAIN=66 / 1326;
 RX MEDLINE=92077439; PubMed=1743521;
 RA Shareck F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
 RT "sequences of three genes specifying xylanases in Streptomyces
 lividans.";
 RL Gene 107:75-82(1991).
 CC - FUNCTION: Contributes to hydrolyze hemicellulose, the major
 CC component of plant cell-walls.
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC - PATHWAY: xylan degradation.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M64553; AAA26836.1; -
 CC EMBL; A25107; CAA01768.1; -
 CC PIR; J05091; J05091.
 DR HSSP; P09850; IXNB.
 DR InterPro; IPR008985; Corn_like_1ec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR InterPro; IPR006311; Tat.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PRO0911; GLHYDRASE11.
 DR TIGRfam; TIGR01409; Tat_signal_seg; 1.
 DR PROSITE; PS00776; GLYCOSTL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSTL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolyase; Glycosidase; Signal.
 FT SIGNAL 1 49
 FT CHAIN 50 240 ENDO-1,4-BETA-XYLANASE C.
 FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;

Query Match 47.2%; Score 503; DB 1; Length 240;
 Best Local Similarity 51.0%; Pred. No. 1.7e-35;
 Matches 98; Conservative 30; Mismatches 54; Indels 10; Gaps 6;

QY 2 TTPGNGYVYVNDGSGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 61
 DB 55 TTPGNGYVYVNDGSGVYITNPGGQFVSVMNSGNFPGKGMQGTGNKYNIFSGSY 109

QY 62 FSGSYVNPNSYLVYVGSRNPLIEYIVENFGYVNPSTGATKLGECTCDGSGVDYITQ 121
 DB 110 FSGSYVNPNSYLVYVGSRNPLIEYIVENFGYVNPSTGATKLGECTCDGSGVDYITQ 167

QY 122 RVNPSIICTATFYQVYVRNHRSSGS-VNTACHPCNAGCLTLGTMVDYIVAVEG 178
 DB 168 RVNPSIICTATFYQVYVRNHRSSGS-VNTACHPCNAGCLTLGTMVDYIVAVEG 227

QY 179 YPSSGSASITVS 190
 DB 228 YPSSGSASITVS 239

RESULT 15
 XYNL BACST STANDARD; PRT; 210 AA.
 AC P45705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 DE (1,4-beta-D-xylan xylanohydrolyase A).
 GN XYNL.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO. 236;
 RA Cho S., Choi Y.;
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
 RT Bacillus stearothermophilus.";
 RL J. Microbiol. Biotechnol. 5:117-124(1995).
 CC [2]
 CC REVISIONS.
 CC STRAIN=NO. 236;
 RA Cho S., Choi Y.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC - PATHWAY: xylan degradation.

CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC

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CC modify and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/annouce/>
CC or send an email to license@isb-sib.ch).

DR	EMBL, U15985; AAB72117.1; -.
DR	HSSP; P09850; 1XNB.
DR	InterPro: IPRO00985; Cons. like lec.g1.
DR	InterPro: IPRO01137; Glyco_hydro_11.
DR	Pfam: PF00457; Glyco_hydro_11; 1.
DR	PRINTS; P00091; GLYTROLASE1.
DR	PROSITE; PS00776; GLYCOSTL_HYDROL_F11_1; 1.
DR	PROSITE; PS00777; GLYCOSTL_HYDROL_F11_2; 1.
KW	Xylan degradation; Hydrolase; signal.
FT	SIGNAL 1
FT	CHAIN 20
FT	ACT SITE 104
FT	ACT SITE 197
SQ	SEQUENCE 210 AA; 22221 MM; 3190CF74C34AAB5 CAC64;

DR EMBL; J15985; AAB72117.1; -.
DR HSBP; P09850; 1XNB.
DR InterPro; IPR008985; Conc like lec gl.
DR InterPro; IPR001137; Glyc hydro 11.
DR Pfam; PF00457; Glyc hydro 11; 1.
DR PRINTS; PR00911; GLYHDLASE11.
DR PROSITE; PS00776; GLYCOSTL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSTL_HYDROL_F11_2; 1.
KW Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1
FT CHAIN 20
FT ACT_SITE 104
FT ACT_SITE 197
SQ SEQUENCE 210 AA; 23221 MW; 3190CF76C34AAB5 CRC64;

DR HSSP; P09850; 1XNB

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DR      InterPro; IPR008985; cons_1ike_1ec_g1
DR      InterPro; IPR0001137; Glyco_hydro_11.
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DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PROSITE: PS00776: GLYCOSYL HYDROLASES; GLYDRLASE1.

DR PROSITE; PS00777; GLYCOSYL_HYD

KW	Hydrolyase; Glycosidase;
FT	POTENTIAL.
SIGNAL	19
ET	1

FT	CHAIN	20	210	ENDO-1,4-BETA-XYLANAS
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PT	ACT_SITE	ACT_SITE	PROTON DONOR (BY SIMILARITY)
PT	104	104	NUCLEOPHILE (BI SIMILARITY):
PT	197	197	

SEQUENCE 210 AA; 23221 MW; 3190CF74C34AAB45 CRC64;

Query Match 47.0%; Score 500.5; DB 1; Leng

Best Local Similarity 51.9%; Pred. No. 2.4e-35;

Matches 94; conservative 30; mismatches 30; errors

14 FYSYWNDDHGGVITYTNGPGGQFSVNWSNSGNFVGCKGWQPGTKNKVINF-SGSYNPNGNS 72

Query Match	47.0%;	Score 500.5;	DB 1;	Length 210;
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Best Local Similarity	51.9%;	Pred. No. 2.4e-35;
Matches	94:	Conservative 30:
		Mismatches 50:
		Indels 7:
		Gaps 54:

MACRES	21	CONDUCTIVITY	201	TEMPERATURE	202	TIME	203	DATE	204	TIME	205	DATE	206	TIME	207	DATE	208	TIME	209	DATE	210	TIME	211	DATE	212	TIME	213	DATE	214	TIME	215	DATE	216	TIME	217	DATE	218	TIME	219	DATE	220	TIME	221	DATE	222	TIME	223	DATE	224	TIME	225	DATE	226	TIME	227	DATE	228	TIME	229	DATE	230	TIME	231	DATE	232	TIME	233	DATE	234	TIME	235	DATE	236	TIME	237	DATE	238	TIME	239	DATE	240	TIME	241	DATE	242	TIME	243	DATE	244	TIME	245	DATE	246	TIME	247	DATE	248	TIME	249	DATE	250	TIME	251	DATE	252	TIME	253	DATE	254	TIME	255	DATE	256	TIME	257	DATE	258	TIME	259	DATE	260	TIME	261	DATE	262	TIME	263	DATE	264	TIME	265	DATE	266	TIME	267	DATE	268	TIME	269	DATE	270	TIME	271	DATE	272	TIME	273	DATE	274	TIME	275	DATE	276	TIME	277	DATE	278	TIME	279	DATE	280	TIME	281	DATE	282	TIME	283	DATE	284	TIME	285	DATE	286	TIME	287	DATE	288	TIME	289	DATE	290	TIME	291	DATE	292	TIME	293	DATE	294	TIME	295	DATE	296	TIME	297	DATE	298	TIME	299	DATE	300	TIME	301	DATE	302	TIME	303	DATE	304	TIME	305	DATE	306	TIME	307	DATE	308	TIME	309	DATE	310	TIME	311	DATE	312	TIME	313	DATE	314	TIME	315	DATE	316	TIME	317	DATE	318	TIME	319	DATE	320	TIME	321	DATE	322	TIME	323	DATE	324	TIME	325	DATE	326	TIME	327	DATE	328	TIME	329	DATE	330	TIME	331	DATE	332	TIME	333	DATE	334	TIME	335	DATE	336	TIME	337	DATE	338	TIME	339	DATE	340	TIME	341	DATE	342	TIME	343	DATE	344	TIME	345	DATE	346	TIME	347	DATE	348	TIME	349	DATE	350	TIME	351	DATE	352	TIME	353	DATE	354	TIME	355	DATE	356	TIME	357	DATE	358	TIME	359	DATE	360	TIME	361	DATE	362	TIME	363	DATE	364	TIME	365	DATE	366	TIME	367	DATE	368	TIME	369	DATE	370	TIME	371	DATE	372	TIME	373	DATE	374	TIME	375	DATE	376	TIME	377	DATE	378	TIME	379	DATE	380	TIME	381	DATE	382	TIME	383	DATE	384	TIME	385	DATE	386	TIME	387	DATE	388	TIME	389	DATE	390	TIME	391	DATE	392	TIME	393	DATE	394	TIME	395	DATE	396	TIME	397	DATE	398	TIME	399	DATE	400	TIME	401	DATE	402	TIME	403	DATE	404	TIME	405	DATE	406	TIME	407	DATE	408	TIME	409	DATE	410	TIME	411	DATE	412	TIME	413	DATE	414	TIME	415	DATE	416	TIME	417	DATE	418	TIME	419	DATE	420	TIME	421	DATE	422	TIME	423	DATE	424	TIME	425	DATE	426	TIME	427	DATE	428	TIME	429	DATE	430	TIME	431	DATE	432	TIME	433	DATE	434	TIME	435	DATE	436	TIME	437	DATE	438	TIME	439	DATE	440	TIME	441	DATE	442	TIME	443	DATE	444	TIME	445	DATE	446	TIME	447	DATE	448	TIME	449	DATE	450	TIME	451	DATE	452	TIME	453	DATE	454
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QY	1	FYSVMNDGHGVYITNPGGQFSVMNSNSGNFVFGKGMQPGKRNKVIWF-SGSYNPNQNS	72
Db	31	YMQVMTDGGKVNANVNGPGSNYSVTWQNTGNFVFGKMTVSGPRKRVITNNGIMRPSGNG	90
QY	73	YLSYGVMSRNPDLIEYIVENFGTYNPSTGATKIGECTDGSVYDIYRTQVNPQSIIGYA	122
Db	91	YLTLYGMRTRALLIEYIVVDSDWGTYP-R-TGNKY-GTVNSDGGTYDIYTRNANASIDGTQ	148
QY	133	TFYVYMSVRRNRHSSG---SVNTACHPCNCAQGLTLG-TMYQYVANEVGFSSGSASIT	188
Db	149	TFQCFWFSVRQSKRFTGSNVSITFSNHYNMRSKNNLTGSSMAYQYLALEGQSSGSRNSVT	208
QY	189	V	189
Db	209	V	209

Db 31 YMQWTDDGGNNNAVNGPGNYSITWQNTGTFVVGKMTVGSPIRVINNAAGIWEISGNG 90

QY 73 YLSVYQWSRNDLIEYIVENFGTYPNSTGATLIGECTCDGSVYDIYRTQRVNPSITIGTA 1322

Db 91 YLTLYGWTARNALIEYYVVDSDWGTYP-TCNYK-GTVNSDGGTYDIYTTMRYNAPSIDGTQ 148

133 TFYQWVSVRNHSSG--SVNTACHENCMAQHGLTLG-TMDYQIVAVEGYFSSGSASIT 188

db 149 TFOEFWSVROSKRPTGSNVISITFSNHVNAWRSGMNI GSSWAYQVLATEGYQSSGRSNVT 208

QY 189 V 189

Db 209 V 209

Search completed: June 30, 2004, 19:40:10
Job time : 8.25 secs

Job time : 8.25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds
(without alignments)
1816.620 Million cell updates/sec

Title: US-09-856-025B-64

Perfect score: 1066
Sequence: 1 QTIQPGTGYNNGRYSTYND.....YQIVAYEGYSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	95.4	223	3	Q02244
2	1005	94.3	223	3	Q02244
3	913	85.6	223	3	Q02244
4	889	83.4	223	3	Q02244
5	860	80.7	223	3	Q02244
6	755.5	70.9	223	3	Q02244
7	733.5	68.8	223	3	Q02244
8	700.5	65.7	223	3	Q02244
9	695.5	65.2	223	3	Q02244
10	681.5	63.9	223	3	Q02244
11	677.5	63.6	223	3	Q02244
12	675.5	63.4	223	3	Q02244
13	675.5	63.4	223	3	Q02244
14	667.5	62.6	223	3	Q02244
15	661.5	62.1	223	3	Q02244
16	641.5	60.2	223	3	Q02244

17	635.5	59.6	194	3	P81536
18	635.5	59.6	230	3	Q81V55
19	632	59.3	221	3	Q9UT02
20	623.5	58.5	223	3	Q9HRH0
21	622.5	58.4	221	3	Q13447
22	620.5	58.2	346	2	Q8VUT4
23	617.5	57.9	283	3	Q96UV7
24	615.5	57.7	221	3	Q00350
25	607.5	56.8	227	3	Q9HGE1
26	605.5	56.8	221	3	P87037
27	595.5	55.9	231	3	Q72A57
28	594.5	55.9	338	2	Q56265
29	594.5	55.8	335	2	Q08346
30	594.5	55.8	335	2	Q9R0M4
31	593.5	55.7	335	2	Q9R0B8
32	591.5	55.5	221	3	Q9CIR1
33	587	55.1	216	3	Q74716
34	578	54.2	228	2	Q59962
35	575.5	54.0	344	2	Q8KXV7
36	569.5	53.4	329	2	Q9RKH9
37	567	53.2	335	16	Q9RKH6
38	547	51.3	191	2	Q9EWH9
39	519.5	48.7	661	2	Q59674
40	515	48.3	352	2	Q84DD2
41	514.5	48.3	361	2	Q52375
42	511.5	48.0	360	2	P77853
43	509.5	47.8	656	2	Q59300
44	506.5	47.5	241	16	Q9R172
45	503	47.2	357	2	Q8VP72

ALIGNMENTS

RESULT 1
Q02244 PRELIMINARY; PRT; 223 AA.
ID Q02244
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Endoxylanase II (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XLN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaeae; Hypocrea.
OX NCBI_TaxID=51453;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=94088442; PubMed=8264524;
RA Saarelaenen R., Paloheimo M., Fagerstrom R., Suominen P.L.,
RA Nevalainen K.M.,
RT Cloning, sequencing and enhanced expression of the Trichoderma reesei
RT endoxylanase II (pI 9) gene xln2.
RL Mol. Gen. Genet. 241:497-503 (1993).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
CC EMBL: S67387; AAB29346.1; -.
CC DR PIR: S39883; S39883.
CC DR HSSP: P36217; 1XVO.
CC DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
CC DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
CC DR InterPro: IPR008985; Cons. like Jec. gl.
CC DR InterPro: IPR001137; Glyco_hydro_11.
CC DR Pfam: PF00457; Glyco_hydro_11; 1.
CC DR PRINTS: PR00911; GLHYDRLASE11.
CC DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC DR GlycoBase: Hydrolase; Xylan degradation.
CC KW Glycosylase; Hydrolase; Xylan degradation.
SQ SEQUENCE 223 AA; 24069 MW; 79668149EADMD22F9 CRC64;

Query Match 95.4%; Score 1017; DB 3; Length 223;
 Best Local Similarity 97.4%; Pred. No. 2, 8e-72;
 Matches 183; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYFYSYWMDHGGVTTNGPGQFSVWNSNSGNFVGKGMQPGTKNKVI 60
 DB OTTGTGTYNNGYFYSYWMDHGGVTTNGPGQFSVWNSNSGNFVGKGMQPGTKNKVI 93
 QY 61 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120
 DB 94 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 153
 QY 121 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQIYAVEGYF 180
 DB 154 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAAQGLTLGTMDOYQIYAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

AC Q99015; PRELIMINARY; PRT; 223 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYN2.
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=QM 6a.
 RA MEDLINE=97076932; PubMed=8975597;
 RA la Grange D.C., Pectorius I.S., Van Zyl W.H.;
 RT "Expression of a trichoderma reesei beta-xylanase gene (XYN2) in
 RT Saccharomyces cerevisiae";
 RL Appl. Environ. Microbiol. 62:1036-1044(1996).
 CC -1- CATALYTIC ACTIVITY: ENDOMYDOLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC -1- LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: U24191; AAB50278.1; -.
 DR HSSP: P36217; IXYO.
 DR GO: GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . . IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; ConA_Like_1ec_91.
 DR InterPro: IPR001137; Glyco_Hydro_11.
 DR Pfam: PF00457; Glyco_Hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Glycosidase; Hydrolyase; Signal; Xylan degradation.
 FT SIGNAL
 FT CHAIN 1 223 POTENTIAL
 FT SIGNAL 34 223 BETA_XYLANASE
 SQ SEQUENCE 223 AA; 23981 MW; F696E545DAC90EB4 CRC64;

Query Match 94.3%; Score 1005; DB 3; Length 223;
 Best Local Similarity 96.3%; Pred. No. 2, 4e-71;
 Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYFYSYWMDHGGVTTNGPGQFSVWNSNSGNFVGKGMQPGTKNKVI 60
 DB OTTGTGTYNNGYFYSYWMDHGGVTTNGPGQFSVWNSNSGNFVGKGMQPGTKNKVI 93
 QY 61 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120

DB 94 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQIYAVEGYF 180

DB 154 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAAQGLTLGTMDOYQIYAVEGYF 213

QY 181 SSGSASITVS 190

DB 214 SSGSASITVS 223

RESULT 3

Q72803 PRELIMINARY; PRT; 223 AA.

AC Q72803; PRELIMINARY; PRT; 223 AA.
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
 OS Trichoderma viride.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YNCC0183;
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.D.,
 RA Yang Z.W.;
 RT "Cloning and characterization of endo-1,4-beta-xylanase from
 RT Trichoderma viride YNCC0183";
 RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY320048; AAF83925.1; -.
 KM Glycosidase; Hydrolyase; Xylan degradation.
 SQ SEQUENCE 223 AA; 24218 MW; F3AF4BE76FA03CAE CRC64;

Query Match 85.6%; Score 913; DB 3; Length 223;
 Best Local Similarity 85.3%; Pred. No. 4, 1e-64;
 Matches 162; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 OTTGTGTYNNGYFYSYWMDHGGVTTNGPGQFSVWNSNSGNFVGKGMQPGTKNKVI 60

DB OTTGTGTYNNGYFYSYWMDHGGVTTNGAGSFSVWNSGNFVGKGMPPSSSRVI 93

QY 61 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 120

DB 94 NFGSYNPNNGNSYLSVYGMGRNPLIEYIVENFGTNPSTGATKLGECTCDGSVYDIYRT 153

QY 121 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTACHFNCAQHGLTLGTMDOYQIYAVEGYF 180

DB 154 QRVNPSIIGTATFYQYWSYVRNRHSSGSVNTAHFNMAAQGLTLGTMDOYQIYAVEGYF 213

QY 181 SSGSASITVS 190

DB 214 SSGSASITVS 223

RESULT 4

Q8U0T4 PRELIMINARY; PRT; 220 AA.

AC Q8U0T4; PRELIMINARY; PRT; 220 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Xylanase.
 OS Trichoderma sp. SY.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=215577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SY;
 RA Min S.Y., Kim B.G., Ahn J.-H.;
 RA "Purification, Characterization, and cDNA Cloning of Xylanase from

QY	Query Match	83.4%	Score 889;	DB 3;	Length 220;
Db	Best Local Similarity	83.2%;	Pred. No. 3, 1e-62;		
	Matches 158;	Conservative 11;	Mismatches 21;	Indels 0;	Gaps 0
QY	1	OTIOGCTGNNNGYFYSVYNDWDGCGYTTNTGPGGQFSVYMSNSGNTFVGGKMGQPGIKAKYI	60		
Db	31	QYIGGTGTGNNNGYFYSVYNDWDGCGYTTNTGAGGGSFVYMSNSGNTFVGGKMGQPGIKAKYI	90		
QY	61	NFGSGYNPNNGSYLSYVYGSRNPLIEYIVENFGYVNPSTGATKLGECCDDSVYDIYRT	120		
Db	91	NFGSGYSPNDNSYLSYVYGSKNPLIEYIVENFGYVNPSTGATKLGEVTLDSVYDIYRT	150		
QY	121	QRYNPSTIIIGTATFFQYVSVYRNHSSSGSVYNTACFNCAGGGLTGTMDYIVAVEGYF	180		
Db	151	QRYNPSTIIIGTATFFQYVSVYRNHSSSGSVYNTACFNCAGGGLTGTMDYIVAVEGYF	210		
QY	181	SSGSASITVS 190			
Db	211	SSGSANINVS 220			

RESULT 5

ID	Q9UVF9	PRELIMINARY;	PRT;	223 AA.
Q9UVF9				
AC	Q9UVF9;			
DT	01-MAY-2000 (TREMblrel. 13, Created)			
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMblrel. 25, Last annotation update)			
DE	Eno-1,4-beta-xyylanase precursor (EC 3.2.1.8)			
OS	Trichoderma viride.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypococreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.			
OX	NCBI_TaxID=5547;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RT	Fuman-Matarasso N., Cohen E., Avni A.;			
RT	Wactions in the Active Site of the Ethylene Inducing Xylanase			
RT	Ellicitor Inhibits the b-1,4-Endoxylanase Activity But Not the			
RT	Ellicitation Activity."			
RL	Submitted (NOV-1998) to the EMBL/Genbank/DBJ databases.			
CC	-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC			
CC	LINKAGES IN XYLANS.			
CC	-1- PATHWAY: XYLAN DEGRADATION.			
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL			
CC	HYDROLASES).			
DR	EMBL; AJ012718; CAB60757.1; -.			
DR	HSSP; P48793; 1XND.			
DR	GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR008985; ConA_like_1ec_1.			
DR	InterPro; IPR001137; Glyco_hydro_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PRO0911; GLHYCDLASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
DR	PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.			
KW	Glycosidase; Hydrolase; Signal; Xylan degradation.			
FT	SIGNAL 1	POTENTIAL		
FT	CHARIN 34			
FT	SEQUENCE 223 AA; 24230 MW; FFB812028FB1212A CQC64;			

Query Match	80.7%	Score 860	DB 3	Length 223
Best Local Similarity	80.5%	Pred. No. 5	9e-60	
Matches 153	Conservative 12	Mismatches 25	Indels 0	Gaps 0

QY	1	QTITQGTGTGNCGYFYASYNNDHGAVTYTNGPCGQFSVWNSNGNFVYSGKMGKQPGTKRKYI	60
DB	34	QTIGGCTFENNNGYYYSYNNDGHSVYTYNCAQGSFSVWANSNGNFVYSGKMGPGSSRYI	93
QY	61	NFSGSYNENGNSYLSVYCGMSRPLIEYIVENFGTYNPSTGATKXEGECTCDGSDYDIYRT	120
DB	94	NFSGSYNENGNSYLSVYCGMSKPLIEYIVENFGTYNPSTGATKXEGEYTSDSQSYDIYRT	153
QY	121	QRVNPSTLTGTATPYQYWSVFRNRHSSGSVNTACHFNCWAQHGTLTGMDYQIVAAVEGYF	180
DB	154	QRVNPSTLTGTATPYQYWSVFRNRHAPARSRLRTTSNMRNLGLTGLTDYQIVAAVEGYF	213
QY	181	SSGSASITVS	190
DB	214	SSGNANINVS	223

ID	Q12580	PRELIMINARY;	PRT;	241 AA.
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, last annotation update)			
DE	Endo-beta-4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).			
OS	Chaetomium gracile.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.			
OX	NCBI_TaxID=47794;			
ON	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96118924; Pubmed=8595661;			
RA	Yoshino S, Oishi M, Moriyama R, Kato M, Tsukagoshi N;			
RT	"Two family G xylanase genes from Chaetomium gracile and their			
RT	expression in Aspergillus nidulans.";			
RL	Curr. Genet. 29;73-80(1995).			
CC	-1- CATALYTIC ACTIVITY: ENDOPOLYSACCHARIDASE OF 1,4-BETA-D-XYLOSIDIC			
CC	LINKAGES IN XYLANS.			
CC	-1- PATHWAY: XYLAN DEGRADATION.			
CC	-1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL			
CC	HYDROLASES).			
DR	EMBL; D49851; AAA08650.1; -			
DR	PIR; S71473; S71473.			
DR	HSP; P36217; IXYO.			
DR	GO; GO:0004553; P:carbohydrate metabolism; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR008965; Consilike_Iec_g1.			
DR	InterPro; IPR001137; Glyco_hydro_11.			
DR	Pfam; PF00457; Glyco_hydro_11; 1.			
DR	PRINTS; PR00911; GLHYDRASE11.			
DR	PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.			
KW	Glycosidase; Hydrolase; Xylan degradation			
QY	SEQUENCE 241 AA; 25564 MW; DCD4B012272F777F CRC64;			
QY	Query Match 70.9%; Score 755.5; DB 3; Length 241;			
QY	Best Local Similarity 72.7%; Pred. No. 1e-51;			
QY	Matches 133; Conservative 20; Mismatches 29; Indels 1; Gaps 1			
Db	7 TGYNNRYFSYNNDDHGCVTYTNGGCGFVYVNSNGNFVGGKMOGCTKKKVIYNSGSY 66			
Db	38 TGYNNRYFSYNNDDHGCVTYTNGGCGFVYVNSNGNFVGGKMOGCTKKKVIYNSGSY 66			
QY	67 NFGNSYLSVYQMSHNPILLEYIVVENFSTYNTSGATKLEGCTDGSVYIYRTORVNP 126			
Db	97 NFGNSYLSVYQMSHNPILLEYIVVENFSTYNTSGATKLEGCTDGSVYIYRTORVNP 126			
QY	127 SIIGITATPQVYVSFRNRHSSGSVNTACHENCAOHGILITGMDYQIVAVEGYFSSGSAS 186			

DB 157 SIEGISTFYQFWSVRNKKSGSVANMAAHFNAMALAGLQGTHTDXYIVATEGGYSSGSAT 216

QY 187 ITV 189

DB 217 VNV 219

RESULT 7

Q871E8 PRELIMINARY; PRT; 293 AA.

ID Q871E8

AC Q871E8

DT 01-JUN-2003 (Tremblrel. 24, Created)

DT 01-JUN-2003 (Tremblrel. 24, last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, last annotation update)

DE Probable endo-1, 4-beta-xylanase B.

GN BGG12.010.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_Taxid=5141;

RN [1]

RP SPOUNCE FROM N.A.

RA Schulte U., Aisin V., Hehse J., Brandt P., Fartmann B., Holland R., Nykatura G., Hoes H.W., Mannhaupt G.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA German Neurospora genome project;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX94027; CAD71059.1; -

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR000254; CBD_fungal.

DR InterPro: IPR008985; ConA like lec.g1.

DR InterPro: IPR001137; Glyco_hydro_11.

DR Pfam; PF00734; CBM_1; 1.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GHYDRLASE11.

DR ProDom; PD001821; CBD_fungal; 1.

DR SMART; SM00236; fcbd; 1.

DR PROSITE; PS00562; CBD_FUNGAL; 1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.

DR GlycoSIDase; Hydrolyase; Xylan degradation.

KW SEQUENCE 293 AA; 30776 MW; D67A61CE65930726 CRC64;

SQ

Query Match 68.8%; Score 733.5; DB 3; Length 293;

Best Local Similarity 69.8%; Pred. No. 6.8e-50;

Matches 128; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYNNGFYFYVNDHGCVYITNGPGQFVSVMNSGNFVGKGMOPGTNKXVINFSGSY 66

DB 42 TGTNGYVYFMTDGGQSVRYTNEAGQYATWSGNNGWVGKGMPEGT-DRTINITGII 100

QY NPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKGECTCDGSDVYDIYTORVNP 126

DB 101 SPNGSHYAVGWRNPLIEYIVENFGTYNPSTGATKGECTCDGSDVYDIYTORVNP 160

QY 127 SIIATATFYQYVSRNRHSSGSVNTACHFNCAOAGLITGTDYQIVANEGYFSSGSAS 186

DB 161 SIDGATFYQYVSRNRHSSGSVNTACHFNCAOAGLITGTDYQIVANEGYFSSGSST 220

QY 187 ITV 189

DB 221 INV 223

RESULT 8

Q871E8 PRELIMINARY; PRT; 261 AA.

AC Q871E8

DT 01-MAR-2003 (Tremblrel. 23, Created)

DT 01-MAR-2003 (Tremblrel. 23, last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, last annotation update)

DE Endoxylanase 11A precursor.

GN XYN11A.

OS Chaetomium thermophilum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

OX NCBI_Taxid=209285;

RN [1]

RP SEQUENCE FROM N.A.

RA Mantyla A., Paloheimo M., Hakola S., Leskinen S., Vehmaandera J., Lantto R., Suominen P.;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ508931; CAD48749.1; -

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; ConA like lec.g1.

DR InterPro: IPR001137; Glyco_hydro_11.

DR Pfam; PF00457; Glyco_hydro_11; 1.

DR PRINTS; PR00911; GHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

KW Signal; Xylan degradation; Hydrolyase; Glycosidase.

FT SIGNAL 1 19

FT CHAIN 20 261

SQ SEQUENCE 261 AA; 27844 MW; 420D625634D707 CRC64;

Query Match 65.7%; Score 700.5; DB 3; Length 261;

Best Local Similarity 64.2%; Pred. No. 2.3e-47;

Matches 122; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY 1 QTI-QPGTVNNGFYFYVNDHGCVYITNGPGQFVSVMNSGNFVGKGMOPGTNKV 59

DB 27 QTLSSATGTHNGYVYFMTDGGQSVRYTNEAGQYATWSGNNGWVGKGMPEGT-DRTINITGII 86

QY 60 INFSGSYNPNNSYLSYVGMGRNPLIEYIVENFGTYNPSTGATKGECTCDGSDVYDIY 119

DB 87 INVTADYRPNNGSHYAVGWRNPLIEYIVENFGTYNPSTGATKGECTCDGSDVYDIY 146

QY 120 TORVNPSTGATFYQYVSRNRHSSGSVNTACHFNCAOAGLITGTDYQIVANEGY 179

DB 147 TORVNPSTGATFYQYVSRNRHSSGSVNTACHFNCAOAGLITGTDYQIVANEGY 206

QY 180 FSSGSASITV 189

DB 207 YSSGSATVNV 216

RESULT 9

Q12579 PRELIMINARY; PRT; 219 AA.

ID Q12579

AC Q12579

DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, last annotation update)

DE Endo-beta-1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN CGXA.

OS Chaetomium gracile.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.

OX NCBI_Taxid=47794;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96118924; PubMed=8595661;

RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;

RT "Two family G xylanase genes from Chaetomium gracile and their expression in Aspergillus nidulans."

RL Cyt. Genet. 29:73-80(1995).

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.


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CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: D49850; BAA08649.1; -.
DR PIR: S71472; S71472.
DR HSSP: P36217; 1XVO.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR InterPro: IPR008985; P:carbohydrate metabolism; IEA.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSite: Glycosylase; Xylan degradation.
SQ SEQUENCE 219 AA; 23324 MW; 4729299E08FD9B4 CRC64;

Query Match 65.2%; Score 695.5; DB 3; Length 219;
Best Local Similarity 67.6%; Pred. No. 4.7e-47;
Matches 125; Conservative 22; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGNNNGFYSSYMNDDHGCVTYTNGPGQPSVWNSNGNFVGGKGMQPGTKNKVINFGSGS 65
DB GTGNNNGFYSSFWTDGGCVTYTNGPGAGGSYSVQWQNGNFGVGGKGMNFGAA -RTINFSGT 94

QY 66 YNPNGNSYLSVGMSPLEIYIVENFGTYNPGSTATKLGECTCDGSVDIYRTQVNPQ 125
DB 95 FSPGNGYLAIVGWTQNPVLEYIVESFGTYDPSSQASKFTGIQQDGSYTTAKTRVNPQ 154

QY 126 PSIIATFYQWVSRRNHRSSGSVNTACHFNCWAQGLTLGTMDOIVAVEGFSSGSA 185
DB 155 PSIEGTFPQWFSVGNHRSSGSVNVAAAFNMAQGLKLSHNYQIVATBSYQSSGSS 214

QY 186 SITVS 190
DB 215 SITVS 219

RESULT 10
Q9HFA4 PRELIMINARY; PRT; 232 AA.
ID Q9HFA4;
AC Q9HFA4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYNCG.
OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_Taxid=5062;
[1]
RP SEQUENCE FROM N.A.
RA Kimura T., Sakka K., Ohmura K.;
RT "Molecular cloning, overexpression, and purification of major xylanase
RT from Aspergillus oryzae."
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYOHLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: AB044941; BAB20794.1; -.
DR PIR: JC7577; JC7577.
DR HSSP: P36217; 1XVO.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; ConA_like_1ec.g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSite: Glycosylase; Xylan degradation.
SQ SEQUENCE 232 AA; 24605 MW; 1F73104751EAS61C CRC64;

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Query Match 63.9%; Score 681.5; DB 3; Length 232;
Best Local Similarity 65.6%; Pred. No. 6.3e-46;
Matches 120; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGNNGFYSSYMNDDHGCVTYTNGPGQPSVWNSNGNFVGGKGMQPGTKNKVINFGSGY 66
DB 50 TGNNGFYSSFWTDGGCVTYTNGNGGSYSVQWQNGNFGVGGKGMNFGS -SRAIFYSGSF 108

QY 67 NPNNGNSYLSVGMSPLEIYIVENFGTYNPGSTATKLGECTCDGSVDIYRTQVNPQ 126
DB 109 NSGNGYLAIVGWTQNPVLEYIVESFGTYDPSSQASKFTGIQQDGSYTTAKTRVNPQ 168

QY 127 PSIIATFYQWVSRRNHRSSGSVNTACHFNCWAQGLTLGTMDOIVAVEGFSSGSA 186
DB 169 SIIGATFYQWVSRRNHRSSGSVNTACHFNCWAQGLTLGTMDOIVAVEGFSSGSA 228

QY 187 ITV 189
DB 229 ITV 231

RESULT 11
Q9C1R2 PRELIMINARY; PRT; 295 AA.
ID Q9C1R2;
AC Q9C1R2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYL5.
OS Fusarium oxysporum f. sp. lycopersici.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_Taxid=59765;
[1]
RP SEQUENCE FROM N.A.
RA Hera C., Gomez-Gomez E., Roncero M.;
RT "Cloning and characterization of two family 11 xylanase genes in
RT Fusarium oxysporum f. sp. lycopersici."
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOMYOHLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XILAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: AF246830; AAK7974.1; -.
DR HSSP: O43097; 1XNA.
DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; ConA_like_1ec.g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PF00457; Glyco_hydro_11.
DR PRINTS: PR00911; GLHYDRLASE11.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoSite: Glycosylase; Xylan degradation.
SQ SEQUENCE 295 AA; 30858 MW; CA441056DCD3C104 CRC64;

Query Match 63.6%; Score 677.5; DB 3; Length 295;
Best Local Similarity 64.1%; Pred. No. 1.7e-45;
Matches 118; Conservative 25; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGNNGFYSSYMNDDHGCVTYTNGPGQPSVWNSNGNFVGGKGMQPGTKNKVINFGSGY 66
DB 40 SGTNNGFYSSWMDGADATYTNBEGGSYSMEKDGANVVGKGMNPG -KARITISGEY 98

QY 67 NPNNGNSYLSVGMSPLEIYIVENFGTYNPGSTATKLGECTCDGSVDIYRTQVNPQ 126
DB 99 KPNNGNSYLSVGMSPLEIYIVESFGTYDPSSQASKFTGIQQDGSYTTAKTRVNPQ 158

QY 127 SIIGATFYQWVSRRNHRSSGSVNTACHFNCWAQGLTLGTMDOIVAVEGFSSGSA 186

```

Db 159 S-DIGTQTCQYWSVRCQHRSTGSDVTGLHFDAMEKAGMKLTHDYCLLATEGYFSSGSSH 218
 QY 187 ITVS 190
 Db 219 MTVS 222

RESULT 12

Q9HEZ0 PRELIMINARY; PRT; 290 AA.

AC Q9HEZ0; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYNB.
 OS Phanerochaete chrysosporium.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Aphyllophorales; Corticiaceae; Phanerochaete.
 OX NCB1_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=ME446;
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301904; AAG44994.1; -.
 DR HSSP; P00725; IAZ6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; ConA_like_deg_gl.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fcbd_1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match

Best Local Similarity 63.4%; Score 675.5; DB 3; Length 290;
 Matches 120; Conservative 25; Mismatches 44; Indels 1; Gaps 1;

QY 1 OTTQPGTNNNGFYSYWNDGHSVYTYNGPGGFSYWNMSNGNPGGKMGWPGTKNYI 60
 Db 34 OSTPAGTGTTNGGTFYSFTWDGGSVYTNNGPAGSYVTWGNANFVAGKMGNGSA-QA1 92
 QY 61 NFSGSYNPNNGSYLSYVGMSRNPILIEYIVENFGTYNPGATKLGECTCGSVYDIYRT 120
 Db 93 SFTANYGPNNGSYLSYVGMSRNPILIEYIVENFGTYNPGATKLGECTCGSVYDIYRT 152
 QY 121 QRVNQPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYF 180
 Db 153 TRVNEPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYF 212
 QY 181 SSGSASITVS 190
 Db 213 SSGSSTVTYN 222

RESULT 13

Q9HEY9

ID Q9HEY9 PRELIMINARY; PRT; 290 AA.

AC Q9HEY9;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XYNB.

OS Phanerochaete chrysosporium.

OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;

OC Aphyllophorales; Corticiaceae; Phanerochaete.

OX NCB1_TaxID=5306;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ME446;
 RA Khan S.N., Loera-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301905; AAG44995.1; -.
 DR HSSP; P00725; IAZ6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; ConA_like_deg_gl.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00734; CBM_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fcbd_1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 290 AA; 30424 MW; 6D1C6415370A689D CRC64;

Query Match

Best Local Similarity 63.4%; Score 675.5; DB 3; Length 290;
 Matches 120; Conservative 25; Mismatches 44; Indels 1; Gaps 1;

QY 1 OTTQPGTNNNGFYSYWNDGHSVYTYNGPGGFSYWNMSNGNPGGKMGWPGTKNYI 60
 Db 34 OSTPAGTGTTNGGTFYSFTWDGGSVYTNNGPAGSYVTWGNANFVAGKMGNGSA-QA1 92
 QY 61 NFSGSYNPNNGSYLSYVGMSRNPILIEYIVENFGTYNPGATKLGECTCGSVYDIYRT 120
 Db 93 SFTANYGPNNGSYLSYVGMSRNPILIEYIVENFGTYNPGATKLGECTCGSVYDIYRT 152
 QY 121 QRVNQPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYF 180
 Db 153 TRVNEPSTIGATFYQYWSVRNRHSSGSVNTACHFNCAOHGLTGTMDYQIVAVEGYF 212
 QY 181 SSGSASITVS 190
 Db 213 SSGSSTVTYN 222

RESULT 14

ID Q00263 PRELIMINARY; PRT; 227 AA.

AC Q00263;

DT 01-NOV-1996 (Tremblrel. 01, Created)

DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-
 xylanase).

GN Ascochyta psi.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina;

OC mitosporic pezizomycotina; Ascochyta.

```

OK NCB1_TaxID=47971;
RN [1]
RP SEQUENCE FROM N.A.
RA Lubeck P.S., Paulin L., Degefu Y., Lubeck M., Collinge D.;
RT "Molecular cloning and DNA sequencing of a xylanase gene from the
RL phytopathogenic fungus Ascochyta blight 1b."
CC Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; Z68891; CA93120.1; -.
DR HSSP; 043097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; Cons_1ike_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYCOSIDase; Hydrolase; Signal; Xylan degradation.
DR SIGNAL 1 19 POTENTIAL.
SQ SEQUENCE 227 AA; 24010 MM; 692AE1FAE035CF0F CRC64;

Query Match 62.1%; Score 667.5; DB 3; Length 227;
Best Local Similarity 64.2%; Pred. No. 7.8e-45;
Matches 124; Conservative 20; Mismatches 44; Indels 5; Gaps 2;

QY 2 T10PQT-----GYNNGYFYSYWNDGAGVTYTNNGPGQGFVSVMNSNGFVGGKMGQPTKXV 57
DB 34 TAAAGTSSGQTHNGCFYSWMDGARAATYTNAGAGSYSVNMKTGMLVGGKMPGA- 92
QY 58 KVINFGSYNPNNGSYLSTVYGSRNPLIEYIVENFGTYPSTGATKLGECTCGSVYDI 117
DB 93 RITVSGTSPSGNSYLAIVGWTNPLIEYIVENFGTYPSSQATVKGSTADGSSYKI 152
QY 118 YRTQVNPQSIIGTATFYQYWSVRNRHRSQSVNTACHFNCMAQHGTLTGMDYQIVAVE 177
DB 153 AQTQRTNPQSIDGTQTFQYWSVRNKRSSGSVMKTHFDMAKMKLGTNHYQIVATE 212
QY 178 GYFSSGSASITVS 190
DB 213 GYFSSGSASQITVN 225

RESULT 15
Q9UVZ3 PRELIMINARY; PRT; 227 AA.
AC Q9UVZ3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XYLI.
OS Setosphaeria turcica.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Setosphaeria.
OX NCB1_TaxID=93612;
RN [1]
RP SEQUENCE FROM N.A.
RA Degefu Y., Paulin L., Peraenen J., Lubeck P.S.;
RT "Cloning, sequencing and expression of a xylanase gene from the maize
RL pathogen Helminthosporium turcicum Pass."
CC Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -1- PATHWAY: XYLAN DEGRADATION.
CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL; AJ238895; CAB52417.1; -.

```

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DR HSSP; 043097; 1YNA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; Cons_1ike_1ec.g1.
DR InterPro; IPR001137; Glyco_hydro_11.
DR Pfam; PF00457; Glyco_hydro_11; 1.
DR PRINTS; PR00911; GLHYDRLASE11.
DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GLYCOSIDase; Hydrolase; Signal; Xylan degradation.
DR SIGNAL 1 19 POTENTIAL.
SQ SEQUENCE 227 AA; 24123 MM; BAE6FC075EE5306E CRC64;

Query Match 62.1%; Score 661.5; DB 3; Length 227;
Best Local Similarity 63.2%; Pred. No. 2.3e-44;
Matches 120; Conservative 22; Mismatches 47; Indels 1; Gaps 1;

QY 1 QTIQPGTGYNNGYFYSYWNDGAGVTYTNNGPGQGFVSVMNSNGFVGGKMGQPTKXV 60
DB 37 QSTPNQEGTHNGCFYSWMDGARAATYTNAGAGSYSVNMKTGMLVGGKMPGA-RTI 95
QY 61 NFGSYNPNNGSYLSTVYGSRNPLIEYIVENFGTYPSTGATKLGECTCGSVYDI 120
DB 96 TISQYINPNNGSYLAIVGWTNPLIEYIVENFGTYPSSQATVKGSTADGSSYKI 155
QY 121 QRTQVNPQSIIGTATFYQYWSVRNRHRSQSVNTACHFNCMAQHGTLTGMDYQIVAVE 180
DB 156 TRTNQPSIDGTQTFQYWSVRNKRSSGSVMKTHFDMAKMKLGTNHYQIVATE 215
QY 181 SSGSASITVS 190
DB 216 SSGSASITVN 225

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Search completed: June 30, 2004, 19:43:41
Job time : 34 secs

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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:33:34 ; Search time 47.5 Seconds

(without alignments)
1130.190 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054
Sequence: 1 QTIQPTGTGNGYFYGYWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1022	97.0	190	3	AAy9736 Mutant T.
2	1019	96.7	190	5	AAE18483 Trichoder
3	1011	95.9	190	5	AAE18482 Trichoder
4	1010	95.8	190	5	AAE18487 Trichoder
5	1009	95.7	190	5	AAE18485 Trichoder
6	1009	95.7	190	5	AAE18484 Trichoder
7	1009	95.7	190	7	AAO30291 Trichoder
8	1009	95.7	190	7	AAO30276 Trichoder
9	1008	95.6	190	5	AAE18486 Trichoder
10	1006	95.4	190	5	AAE18472 Trichoder
11	1006	95.4	190	7	AAO30287 Trichoder
12	1003	95.2	190	5	AAE18476 Trichoder
13	1003	95.2	190	5	AAE18488 Trichoder
14	1002	95.1	190	5	AAE18489 Trichoder
15	1001	95.0	190	7	AAO30292 Trichoder
16	1001	95.0	190	7	AAO30277 Trichoder
17	1000	94.9	190	5	AAE18475 Trichoder
18	1000	94.9	190	7	AAE18474 Trichoder
19	1000	94.9	190	7	AAO30288 Trichoder
20	999	94.8	190	5	AAE18473 Trichoder
21	997	94.6	190	5	AAE18478 Trichoder
22	997	94.6	190	5	AAE18481 Trichoder
23	997	94.6	190	7	AAO30278 Trichoder
24	997	94.6	190	7	AAO30289 Trichoder
25	996	94.5	190	5	AAE18480 Trichoder

26	996	94.5	190	5	AAE18477 Trichoder
27	996	94.5	190	7	AAO30290 Trichoder
28	995	94.4	190	5	AAE18490 Trichoder
29	995	94.4	190	5	AAE18479 Trichoder
30	994	94.3	190	7	AAO30281 Trichoder
31	992	94.1	190	7	AAO30282 Trichoder
32	992	94.1	190	7	AAO30283 Trichoder
33	987	93.6	190	5	AAE18491 Trichoder
34	986	93.5	190	2	AAW60743 Xylanase
35	986	93.5	190	3	AAy9680 T. reesei
36	986	93.5	190	5	AAE18452 Trichoder
37	986	93.5	190	7	AAO30259 Trichoder
38	986	93.5	223	2	AAAR47122 PI 9.0 en
39	986	93.5	223	2	AAW67567 T. reesei
40	985	93.5	190	7	AAO30284 Trichoder
41	985	93.5	223	2	AAW57422 Amino aci
42	984	93.4	190	3	AAy9735 Mutant T.
43	984	93.4	190	5	AAE18494 Trichoder
44	983	93.3	190	5	AAE18470 Trichoder
45	983	93.3	190	5	AAE18495 Trichoder

ALIGNMENTS

RESULT 1
ID AAY9736 standard; protein; 190 AA.

AC AAY9736;
XX
XX
DT 12-SEP-2003 (revised)
DT 28-SEP-2000 (first entry)
XX
DE Mutant T. reesei xylanase, Trx-DS8.
XX
XX
KW Xylanase; animal feed; digestion efficiency; thermostable;
KW feed pelleting; enzyme; mutant; muten; Xyn A; Xyn B; Xyn C; Xyn I;
KW Xyn II.
OS Hypocrea jecorina.
XX
XX
EN WO200029587-A1.
XX
XX
PD 25-MAY-2000.
XX
XX
PF 16-NOV-1999; 99WO-CA001093.
XX
XX
PR 16-NOV-1998; 98US-0108504P.
XX
XX
PA (IOGE-) IOGEN CORP.
XX
XX
PI Sung WL, Tolan JS;
XX
XX
DR WPI; 2000-387799/33.
XX
XX
PT Thermostable xylanases useful for preparing animal feeds especially
PT poultry or swine feed, exhibits optimal activity under physiological
conditions.
XX
XX
PS Claim 18; Page; 86pp; English.
CC Xylanase enzymes are added to animal feeds to increase the efficiency of
digestion and assimilation of nutrients. Xylanases are preferentially
CC added during the feed pelleting process. To survive the pelleting process
CC and to have optimum activity in the animal, the xylanase needs to have
CC high thermostability, with optimum activity at physiological pH and
CC temperature. Xylanase Xyn II, from Trichoderma reesei, is a xylanase
CC family II member. The xylanases of family II have several properties
CC suitable for feed applications, however, they lack the thermostability
CC required to survive food pelleting. The present sequence was used to
CC identify non-conserved residues in family II xylanases which could be
CC mutated to introduce desirable properties e.g. thermostability. As a

XX (CANA) NAT RES COUNCIL CANADA.
 PA
 XX
 PI Sung WL;
 XX
 XX WPI; 2002-171435/22.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 PS
 XX Claim 42; Page; 109pp; English.
 PS
 XX The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
 CC specification but is derived from wild type xylanase referred as SEQ ID
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
 XX
 SQ Sequence 190 AA;

Query Match 95.8%; Score 1011; DB 5; Length 190;
 Best Local Similarity 97.4%; Pred. No. 1.2e-85;
 Matches 188; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNDGSGVMTLGPQGFVSVMNSGDFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYHNGYFYSYNDGSGVMTLGPQGFVSVMNSGDFVGKGMQPGTKNKVI 60
 QY 61 NFGSYNPNNGNSLYAVGWSRNPLIEYIYVENFGTYPSTGATLGEVTCDSYVDIYRT 120
 DB 61 NFGSYNPNNGNSLYAVGWSRNPLIEYIYVENFGTYPSTGATLGEVTCDSYVDIYRT 120
 QY 121 QRVNAPSEIGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTDYQIYAVEGYF 180
 DB 121 QRVNAPSEIGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 4
 AAE18487
 ID AAE18487 standard; protein; 190 AA.
 XX
 AC AAE18487;
 XX
 XX

DE 16-MAY-2002 (first entry)
 XX
 XX Trichoderma reesei xylanase mutant, Trx-HML-APAE.
 XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutein.
 XX
 OS Hypocrea jecorina.
 OS Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 10
 FT /note= "Wild type Asn substituted with His"
 FT Misc-difference 27
 FT /note= "Wild type Tyr substituted with Met"
 FT Misc-difference 29
 FT /note= "Wild type Asn substituted with Leu"
 FT Misc-difference 75
 FT /note= "Wild type Ser substituted with Ala"

FT Misc-difference 105
 FT /note= "Wild type Leu substituted with Arg"
 FT Misc-difference 125
 FT /note= "Wild type Gln substituted with Ala"
 FT Misc-difference 129
 FT /note= "Wild type Ile substituted with Glu"
 XX
 XX WO200192487-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 31-MAY-2001; 2001WO-CA000769.
 XX
 XX 31-MAY-2000; 2000US-0213803P.
 XX
 XX (CANA) NAT RES COUNCIL CANADA.
 XX
 XX Sung WL;
 XX
 XX WPI; 2002-171435/22.
 XX
 XX
 XX Modified xylanase exhibiting increased thermostability and
 XX alkalophilicity useful for industrial processing e.g. for pulp
 XX manufacturing.
 PS
 XX Claim 42; Page; 109pp; English.

The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improved digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
 CC specification but is derived from wild type xylanase referred as SEQ ID
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
 XX
 SQ Sequence 190 AA;

Query Match 95.8%; Score 1010; DB 5; Length 190;
 Best Local Similarity 96.8%; Pred. No. 1.5e-85;
 Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNDGSGVMTLGPQGFVSVMNSGDFVGKGMQPGTKNKVI 60
 DB 1 QTIQPGTGYHNGYFYSYNDGSGVMTLGPQGFVSVMNSGDFVGKGMQPGTKNKVI 60
 QY 61 NFGSYNPNNGNSLYAVGWSRNPLIEYIYVENFGTYPSTGATLGEVTCDSYVDIYRT 120
 DB 61 NFGSYNPNNGNSLYAVGWSRNPLIEYIYVENFGTYPSTGATLGEVTCDSYVDIYRT 120
 QY 121 QRVNAPSEIGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTDYQIYAVEGYF 180
 DB 121 QRVNAPSEIGTATFYQWVSRRNRHSSGSVNTACHFNAMAQGLTLGTDYQIYAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 5
 AAE18485
 ID AAE18485 standard; protein; 190 AA.
 XX
 AC AAE18485;
 XX
 XX

DE 16-MAY-2002 (first entry)
 XX
 XX Trichoderma reesei xylanase mutant, Trx-HML-AHAE.
 XX
 KW Modified xylanase; thermostability; alkalophilicity; industrial process;
 KW

KM pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.
 XX Hypocrea jecorina.
 OS Synthetic.
 XX

Key Location/Qualifiers

FT Misc-difference 10 /note= "Wild type Asn substituted with His"
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
 FT Misc-difference 75 /note= "Wild type Ser substituted with Ala"
 FT Misc-difference 105 /note= "Wild type Leu substituted with His"
 FT Misc-difference 125 /note= "Wild type Gln substituted with Ala"
 FT Misc-difference 129 /note= "Wild type Ile substituted with Glu"
 FT

WO200192487-A2.

06-DEC-2001.

31-MAY-2001; 2001WO-CA000769.

31-MAY-2000; 2000US-0213803P.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

WPI; 2002-171435/22.

Modified xylanase exhibiting increased thermostability and alkalophilicity useful for industrial processing e.g. for pulp manufacturing.

Claim 42; Page; 109pp; English.

XX The present invention relates to a modified xylanase exhibiting increased thermostability and alkalophilicity. Modified xylanase is useful in industrial process such as pulp manufacturing. Modified xylanase is also useful for bleaching of pulp, processing of precision devices and improving digestibility of poultry and swine feed. Modified xylanase has exhibits improved thermostability and/or alkalophilicity in comparison to corresponding native xylanase. The present sequence is not shown in the specification but is derived from wild type xylanase referred as SEQ ID NO: 16 (AAE18452) and shown in page 80-81 of the specification

Sequence 190 AA;

Query Match 95.7%; Score 1009; DB 5; Length 190;

Best Local Similarity 96.8%; Pred. No. 1.9e-85; Indels 0; Gaps 0;

Matches 184; Conservative 2; Mismatches 4;

QY 1 QTIQGTGNGYHYGYWMDHGGVMTLPGGQPSYVNSGDPYVGKGMOPGTAKYI 60
 DB 1 QTIQGTGNGYHYGYWMDHGGVMTLPGGQPSYVNSGDPYVGKGMOPGTAKYI 60
 QY 61 NFSGSYNPNSYIYVNGSRNPILEYITVENFGTNPISGAKLGEVTCDSVDIYKT 120
 DB 61 NFSGSYNPNSYIYVNGSRNPILEYITVENFGTNPISGAKLGEVTCDSVDIYKT 120
 QY 61 NFSGSYNPNSYIYVNGSRNPILEYITVENFGTNPISGAKLGEVTCDSVDIYKT 120
 DB 61 NFSGSYNPNSYIYVNGSRNPILEYITVENFGTNPISGAKLGEVTCDSVDIYKT 120
 QY 121 QRVNAPSIEGTATFYQYVSWVRNRSSGVTACHPNARQGLTLGTMDYQIVAVEGYF 180
 DB 121 QRVNAPSIEGTATFYQYVSWVRNRSSGVTACHPNARQGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGASITVS 190
 DB 181 SSGASITVS 190

DB 181 SSGASITVS 190

RESULT 6

AAE18484

ID AAE18484 standard; protein; 190 AA.

AAE18484;

16-MAY-2002 (first entry)

Trichoderma reesei xylanase mutant, Trx-HWL-CRAE.

Modified xylanase; thermostability; alkalophilicity; industrial process; pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

Hypocrea jecorina.

OS Synthetic.

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Query Match 95.7%; Score 1009; DB 5; Length 190;

Best Local Similarity 96.8%; Pred. No. 1.9e-85; Indels 0; Gaps 0;

Matches 184; Conservative 1; Mismatches 5;

QY 1 QTIQGTGNGYHYGYWMDHGGVMTLPGGQPSYVNSGDPYVGKGMOPGTAKYI 60

DB 1 QTIQGTGNGYHYGYWMDHGGVMTLPGGQPSYVNSGDPYVGKGMOPGTAKYI 60

QY 61 NFSGSYNPNSYIYVNGSRNPILEYITVENFGTNPISGAKLGEVTCDSVDIYKT 120


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QY 1 QTIOPGTGYNHGYFYSYWNDDHGGVTMTLGRGQFVSVMNSGDFYGGKMGQGTGNKYI 60
Db 1 QTIOPGTGYNHGYFYSYWNDDHGGVTMTLGRGQFVSVMNSGDFYGGKMGQGTGNKYI 60
QY 61 NFSGSYNPNNGNSYLGVTGMSRNPLIEYIYVENFGTYPSTGATKRGVTSDSGVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLGVTGMSRNPLIEYIYVENFGTYPSTGATKRGVTSDSGVYDIYRT 120
QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQGLTLGTMDOYIVAVEGYF 180
Db 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 7
AAO30291
ID AAO30291 standard; protein; 190 AA.
XX
AC AAO30291;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (Trx-HML-GRAB).
XX
KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
OS Hypocrea jecorina.
XX
SY Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10 /note= "Wild type Asn substituted with His"
FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"
FT Misc-difference 105 /note= "Wild type Leu substituted with Arg"
FT Misc-difference 125 /note= "Wild type Ile substituted with Glu"
FT Misc-difference 129 /note= "Wild type Gln substituted with Ala"
FT Misc-difference 129 /note= "Wild type Ile substituted with Glu"
XX
PN WO2003046169-A2.
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2002; 2002WO-CA001758.
XX
PR 21-NOV-2001; 2001US-00990874.
XX
PA (CANA ) NAT RES COUNCIL CANADA.
XX
PI Sung WL;
XX
DR WPI; 2003-513647/48.
XX
PT Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native Trichoderma reesei xylanase from Trichoderma reesei.
XX
PS Example 1; Page; 105pp; English.
XX
CC The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It

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CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AAO30259)
XX
SQ Sequence 190 AA;
XX
Query Match 95.7%; Score 1009; DB 7; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.9e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 QTIOPGTGYNHGYFYSYWNDDHGGVTMTLGRGQFVSVMNSGDFYGGKMGQGTGNKYI 60
Db 1 QTIOPGTGYNHGYFYSYWNDDHGGVTMTLGRGQFVSVMNSGDFYGGKMGQGTGNKYI 60
QY 61 NFSGSYNPNNGNSYLGVTGMSRNPLIEYIYVENFGTYPSTGATKRGVTSDSGVYDIYRT 120
Db 61 NFSGSYNPNNGNSYLGVTGMSRNPLIEYIYVENFGTYPSTGATKRGVTSDSGVYDIYRT 120
QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQGLTLGTMDOYIVAVEGYF 180
Db 121 QRVNAPSIEGTATFYQYWSVRNRHSSGVSNTACHFNMAQGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 8
AAO30276
ID AAO30276 standard; protein; 190 AA.
XX
AC AAO30276;
XX
DT 03-SEP-2003 (first entry)
XX
DE Trichoderma reesei xylanase II mutant protein (Trx-HML-AHAE).
XX
KM Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
XX
KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
XX
OS Hypocrea jecorina.
XX
SY Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 10 /note= "Wild type Asn substituted with His"
FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
FT Misc-difference 75 /note= "Wild type Ser substituted with Ala"
FT Misc-difference 105 /note= "Wild type Leu substituted with His"
FT Misc-difference 125 /note= "Wild type Ile substituted with Glu"
FT Misc-difference 129 /note= "Wild type Gln substituted with Ala"
FT Misc-difference 129 /note= "Wild type Ile substituted with Glu"
XX
PN WO2003046169-A2.
XX
PD 05-JUN-2003.
XX
PF 20-NOV-2002; 2002WO-CA001758.
XX
PR 21-NOV-2001; 2001US-00990874.
XX
PA (CANA ) NAT RES COUNCIL CANADA.
XX
PI Sung WL;
XX

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XX WP1; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermostability, alkalophilicity and expression efficiency. In comparison
PT to a corresponding native xylanase from *Trichoderma reesei*.

XX Claim 7; Page; 105pp; English.

CC The invention relates to modified xylanase enzyme which exhibits improved
CC thermostability, alkalophilicity and expression efficiency. In comparison
CC to a corresponding native *Trichoderma reesei* xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is *Trichoderma reesei* xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC *Trichoderma reesei* wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AA030259).

XX Sequence 190 AA;

Query Match 95.7%; Score 1009; DB 7; Length 190;
Best Local Similarity 96.8%; Pred. No. 1.9e-85;
Matches 184; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYYSYVNDGSGVTWTLGPGGQFSYVNSGDFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGHNGYFYYSYVNDGSGVTWTLGPGGQFSYVNSGDFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGMNSRNPLEYIVENFGTVPNSGATKLGELVTCDSYVDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGMNSRNPLEYIVENFGTVPNSGATKLGELVTCDSYVDIYRT 120
QY 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 9

AAE18486 ID AAE18486 standard; protein; 190 AA.

XX AAE18486;

XX 16-MAY-2002 (first entry)

XX *Trichoderma reesei* xylanase mutant, Trx-HML-GHAE.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

XX *Hypocrea jecorina*.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 10 /note= "Wild type Asn substituted with His"
FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"
FT Misc-difference 105 /note= "Wild type Leu substituted with His"
FT Misc-difference 125 /note= "Wild type Gln substituted with Ala"
FT Misc-difference 129

FT /note= "Wild type Ile substituted with Glu"

XX WO200192487-A2.

XX 06-DEC-2001.

XX 31-MAY-2001; 2001MO-CA000769.

XX 31-MAY-2000; 2000US-0213803P.

XX (CANADA) NAT RES COUNCIL CANADA.

XX Sung WL;

XX WP1; 2002-171435/22.

PT Modified xylanase exhibiting increased thermostability and
PT alkalophilicity useful for industrial processing e.g. for pulp
PT manufacturing.

XX Claim 42; Page; 109pp; English.

CC The present invention relates to a modified xylanase exhibiting increased
CC thermostability and alkalophilicity. Modified xylanase is useful in
CC industrial process such as pulp manufacturing. Modified xylanase is also
CC useful for bleaching of pulp, processing of precision devices and
CC improved performance at conditions of high temperature and pH and
CC exhibits improved thermostability and/or alkalophilicity in comparison to
CC corresponding native xylanase. The present sequence is *Trichoderma reesei*
CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
CC specification but is derived from wild type xylanase referred as SEQ ID
CC NO: 16 (AAE18452) and shown in page 80-81 of the specification

XX Sequence 190 AA;

Query Match 95.6%; Score 1008; DB 5; Length 190;
Best Local Similarity 96.8%; Pred. No. 2.4e-85;
Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYYSYVNDGSGVTWTLGPGGQFSYVNSGDFVGGKMGQPGTKNKVI 60
DB 1 QTIQPGTGHNGYFYYSYVNDGSGVTWTLGPGGQFSYVNSGDFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGNSYLSYVGMNSRNPLEYIVENFGTVPNSGATKLGELVTCDSYVDIYRT 120
DB 61 NFSGSYNPNNGNSYLSYVGMNSRNPLEYIVENFGTVPNSGATKLGELVTCDSYVDIYRT 120
QY 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180
DB 121 QRVNAPSIEGTATFYQYVSVRRNRRSSGSVNTACHFNMAOQGLTGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 10

AAE18472 ID AAE18472 standard; protein; 190 AA.

XX AAE18472;

XX 16-MAY-2002 (first entry)

XX *Trichoderma reesei* xylanase mutant, Trx-HML.

XX Modified xylanase; thermostability; alkalophilicity; industrial process;
KW pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

XX *Hypocrea jecorina*.
OS Synthetic.

FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
 XX
 PN W0200192487-A2.
 XX
 PD 06-DEC-2001.
 XX
 PE 31-MAY-2001; 2001MO-CA000769.
 XX
 PR 31-MAY-2000; 2000US-0213803P.
 XX
 PA (CANADA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 DR WPI; 2002-171435/22.
 XX
 PT Modified xylanase exhibiting increased thermostability and
 PT alkalophilicity useful for industrial processing e.g. for pulp
 PT manufacturing.
 XX
 PS Claim 7; Page; 109pp; English.
 XX
 CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermophilicity and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
 CC specification but is derived from wild type xylanase referred as SEQ ID
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
 XX
 SO Sequence 190 AA;
 Query Match 95.4%; Score 1006; DB 5; Length 190;
 Best Local Similarity 96.8%; Pred. No. 3.6e-85;
 Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 OTIQPGTGHNGYFYSYVNDGHSVMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60
 DB 1 OTIQPGTGHNGYFYSYVNDGHSVMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 QY 121 QRVNAPSIIEGTATFYQVWSVRNRHRSQSVNTACHFNAQAQGLTLGTM DYQIVAVEGYF 180
 DB 121 QRVNAPSIIEGTATFYQVWSVRNRHRSQSVNTACHFNAQAQGLTLGTM DYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190
 RESULT 11
 AAO30287
 ID AAO30287 standard; protein; 190 AA.
 XX
 AC AAO30287;
 XX
 DT 03-SEP-2003 (first entry)
 XX
 DE Trichoderma reesei xylanase II mutant protein (Trx-HML).
 XX

KW Xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 KW pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutein.
 XX
 OS Hypocrea jecorina.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 10 /note= "Wild type Asn substituted with His"
 FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"
 FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"
 XX
 PN W02003046169-A2.
 XX
 PD 05-JUN-2003.
 XX
 PE 20-NOV-2002; 2002MO-CA001758.
 XX
 PR 21-NOV-2001; 2001US-00990874.
 XX
 PA (CANADA) NAT RES COUNCIL CANADA.
 XX
 PI Sung WL;
 DR WPI; 2003-513647/48.
 XX
 PT Novel modified xylanase useful in industrial process, exhibits improved
 PT thermostability, alkalophilicity and expression efficiency, in comparison
 PT to a corresponding native xylanase from Trichoderma reesei.
 XX
 PS Example 1; Page; 105pp; English.
 XX
 CC The invention relates to modified xylanase enzyme which exhibits improved
 CC thermostability, alkalophilicity and expression efficiency, in comparison
 CC to a corresponding native Trichoderma reesei xylanase (Trx). The modified
 CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
 CC is useful for the bleaching of pulp, processing of precision devices and
 CC for improving digestibility of poultry and swine feed. The present
 CC sequence is Trichoderma reesei xylanase II mutant protein. Note: This
 CC sequence is not shown in the specification but is derived from
 CC Trichoderma reesei wild type xylanase II protein shown as SEQ ID NO: 16
 CC in figure 2 of the specification (AAO30259)
 XX
 SO Sequence 190 AA;
 Query Match 95.4%; Score 1006; DB 7; Length 190;
 Best Local Similarity 96.8%; Pred. No. 3.6e-85;
 Matches 184; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 OTIQPGTGHNGYFYSYVNDGHSVMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60
 DB 1 OTIQPGTGHNGYFYSYVNDGHSVMTLGGGQFVSVMNSGDPFGKGMQPGTKNKVI 60
 QY 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTCDGSVYDIYRT 120
 DB 61 NFSGSYNPNNGNSYLSVYGMSRNPLEYIYVENFGTYPSTGATKLGVTSDGSVYDIYRT 120
 QY 121 QRVNAPSIIEGTATFYQVWSVRNRHRSQSVNTACHFNAQAQGLTLGTM DYQIVAVEGYF 180
 DB 121 QRVNAPSIIEGTATFYQVWSVRNRHRSQSVNTACHFNAQAQGLTLGTM DYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190
 RESULT 12
 AAE18476
 ID AAE18476 standard; protein; 190 AA.
 XX
 AC AAE18476;
 XX

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XX 16-MAY-2002 (first entry)
DE Trichoderma reesei xylanase mutant, Trx-HML-75A.
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutcin.
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Msc-difference 10 /note= "wild type Asn substituted with His"
FT Msc-difference 27 /note= "wild type Tyr substituted with Met"
FT Msc-difference 29 /note= "wild type Asn substituted with Leu"
FT Msc-difference 75 /note= "wild type Ser substituted with Ala"
FT Msc-difference 75 /note= "wild type Ser substituted with Ala"
XX WO200192487-A2.
XX 06-DEC-2001.
XX 31-MAY-2001; 2001WO-CA000769.
XX 31-MAY-2000; 2000US-0213803P.
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX WPI; 2002-171435/22.
XX Modified xylanase exhibiting increased thermostability and
XX alkalophilicity useful for industrial processing e.g. for pulp
XX manufacturing.
XX
XX Claim 42; Page; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX useful for bleaching of pulp, processing of precision devices and
XX improving digestibility of poultry and swine feed. Modified xylanase has
XX improved performance at conditions of high temperature and pH and
XX exhibits improved thermophilicity and/or alkalophilicity in comparison to
XX corresponding native xylanase. The present sequence is Trichoderma reesei
XX xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX specification but is derived from wild type xylanase referred as SEQ ID
XX NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX
XX Sequence 190 AA;
XX
XX Query Match 95.2%; Score 1003; DB 5; Length 190;
XX Best Local Similarity 96.3%; Pred. No. 6.9e-85;
XX Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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DB 181 SSGSASITVS 190
RESULT 13
AAE18488
ID AAE18488 standard; protein. 190 AA.
XX
XX AAE18488;
XX
XX 16-MAY-2002 (first entry)
XX
XX Trichoderma reesei xylanase mutant, Trx-HML-GPRAE.
XX
XX Modified xylanase; thermostability; alkalophilicity; industrial process;
XX pulp manufacture; poultry; swine feed; enzyme; mutant; mutcin.
XX Hypocrea jecorina.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Msc-difference 10 /note= "wild type Asn substituted with His"
FT Msc-difference 27 /note= "wild type Tyr substituted with Met"
FT Msc-difference 29 /note= "wild type Asn substituted with Leu"
FT Msc-difference 75 /note= "wild type Ser substituted with Gly"
FT Msc-difference 104 /note= "wild type Lys substituted with Pro"
FT Msc-difference 105 /note= "wild type Leu substituted with Arg"
FT Msc-difference 125 /note= "wild type Gln substituted with Ala"
FT Msc-difference 129 /note= "wild type Ile substituted with Glu"
XX WO200192487-A2.
XX 06-DEC-2001.
XX 31-MAY-2001; 2001WO-CA000769.
XX 31-MAY-2000; 2000US-0213803P.
XX (CANA ) NAT RES COUNCIL CANADA.
XX
XX Sung WL;
XX WPI; 2002-171435/22.
XX Modified xylanase exhibiting increased thermostability and
XX alkalophilicity useful for industrial processing e.g. for pulp
XX manufacturing.
XX
XX Claim 42; Page; 109pp; English.
XX
XX The present invention relates to a modified xylanase exhibiting increased
XX thermostability and alkalophilicity. Modified xylanase is useful in
XX industrial process such as pulp manufacturing. Modified xylanase is also
XX useful for bleaching of pulp, processing of precision devices and
XX improving digestibility of poultry and swine feed. Modified xylanase has
XX improved performance at conditions of high temperature and pH and
XX exhibits improved thermophilicity and/or alkalophilicity in comparison to
XX corresponding native xylanase. The present sequence is Trichoderma reesei
XX xylanase (Trx) mutant. Note: The present sequence is not shown in the
XX specification but is derived from wild type xylanase referred as SEQ ID
XX NO: 16 (AAE18452) and shown in page 80-81 of the specification
XX
XX Sequence 190 AA;
XX
XX Query Match 95.2%; Score 1003; DB 5; Length 190;
XX Best Local Similarity 96.3%; Pred. No. 6.9e-85;

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Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNNGYFYSYWMDGCGVMTLGPQGQFSVWMSNGDFVGGKMQPTKKNYI 60
 DB 1 QTIOPGTGYNNGYFYSYWMDGCGVMTLGPQGQFSVWMSNGDFVGGKMQPTKKNYI 60
 QY 61 NFGSGYNPNNGSYLVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120
 DB 61 NFGSGYNPNNGSYLVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120
 QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
 DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 14

AAE18489 standard; protein; 190 AA.

AAE18489;
 16-MAY-2002 (first entry)

Trichoderma reesei xylanase mutant, Trx-HML-GPHAE.

Modified xylanase; thermostability; alkalophilicity; industrial process;
 pulp manufacture; poultry; swine feed; enzyme; mutant; mutain.

Hypocrea jecorina.
 Synthetic.

Key Location/Qualifiers

FT Misc-difference 10 /note= "Wild type Asn substituted with His"

FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"

FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"

FT Misc-difference 75 /note= "Wild type Ser substituted with Gly"

FT Misc-difference 104 /note= "Wild type Lys substituted with Pro"

FT Misc-difference 105 /note= "Wild type Leu substituted with His"

FT Misc-difference 125 /note= "Wild type Gln substituted with Ala"

FT Misc-difference 129 /note= "Wild type Ile substituted with Glu"

W0200192487-A2.

06-DEC-2001.

31-MAY-2001; 2001WO-CA000769.

31-MAY-2000; 2000US-0213803P.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

WPI; 2002-171435/22.

Modified xylanase exhibiting increased thermostability and
 alkalophilicity useful for industrial processing e.g. for pulp
 manufacturing.

Claim 42; Page; 109pp; English.

CC The present invention relates to a modified xylanase exhibiting increased
 CC thermostability and alkalophilicity. Modified xylanase is useful in
 CC industrial process such as pulp manufacturing. Modified xylanase is also
 CC useful for bleaching of pulp, processing of precision devices and
 CC improving digestibility of poultry and swine feed. Modified xylanase has
 CC improved performance at conditions of high temperature and pH and
 CC exhibits improved thermostability and/or alkalophilicity in comparison to
 CC corresponding native xylanase. The present sequence is Trichoderma reesei
 CC xylanase (Trx) mutant. Note: The present sequence is not shown in the
 CC specification but is derived from wild type xylanase referred as SEQ ID
 CC NO: 16 (AAE18452) and shown in page 80-81 of the specification
 SQ Sequence 190 AA;

Query Match 95.1%; Score 1002; DB 5; Length 190;
 Best Local Similarity 96.3%; Pred No. 8.5e-85;
 Matches 183; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNNGYFYSYWMDGCGVMTLGPQGQFSVWMSNGDFVGGKMQPTKKNYI 60
 DB 1 QTIOPGTGYNNGYFYSYWMDGCGVMTLGPQGQFSVWMSNGDFVGGKMQPTKKNYI 60

QY 61 NFGSGYNPNNGSYLVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120
 DB 61 NFGSGYNPNNGSYLVGWSRNPLEYIYVENFGTYNPSTGATKGEVTCDSVYDIYRT 120

QY 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180
 DB 121 QRVNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTGTMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 15

AAO30292 standard; protein; 190 AA.

AAO30292;

03-SEP-2003 (first entry)

Trichoderma reesei xylanase II mutant protein (Trx-H-11D-ML).

xylanase; thermophilic; alkalophilic; pulp bleaching; industrial;
 pulp manufacture; poultry feed; swine feed; enzyme; mutant; mutain.

Hypocrea jecorina.
 Synthetic.

Key Location/Qualifiers

FT Misc-difference 10 /note= "Wild type Asn substituted with His"

FT Misc-difference 11 /note= "Wild type Asn substituted with Asp"

FT Misc-difference 27 /note= "Wild type Tyr substituted with Met"

FT Misc-difference 29 /note= "Wild type Asn substituted with Leu"

W02003046169-A2.

05-JUN-2003.

20-NOV-2002; 2002WO-CA001758.

21-NOV-2001; 2001US-00990874.

(CANADA) NAT RES COUNCIL CANADA.

Sung WL;

DR WPI; 2003-513647/48.

XX Novel modified xylanase useful in industrial process, exhibits improved
PT thermophilicity, alkalophilicity and expression efficiency, in comparison
PT to a corresponding native xylanase from *Trichoderma reesei*.
XX

PS Example 1; Page; 105pp; English.

XX The invention relates to modified xylanase enzyme which exhibits improved
CC thermophilicity, alkalophilicity and expression efficiency, in comparison
CC to a corresponding native *Trichoderma reesei* xylanase (Trx). The modified
CC xylanase is useful in an industrial process e.g. pulp manufacturing. It
CC is useful for the bleaching of pulp, processing of precision devices and
CC for improving digestibility of poultry and swine feed. The present
CC sequence is *Trichoderma reesei* xylanase II mutant protein. Note: This
CC sequence is not shown in the specification but is derived from
CC *Trichoderma reesei* wild type xylanase II protein shown as SEQ ID NO: 16
CC in figure 2 of the specification (AA030259)
XX

SQ Sequence 190 AA;

Query March 95.0%; Score 1001; DB 7; Length 190;
Best Local Similarity 96.3%; Pred. No. 1.1e-84;
Matches 183; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```
QY 1 QTIQPTGYHNGYFYSYWMDHGVTWTLGPGGQFSYVMSNSGDFVGGKGMQPGTKNKYI 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QTIQPTGYHNGYFYSYWMDHGVTWTLGPGGQFSYVMSNSGDFVGGKGMQPGTKNKYI 60

QY 61 NFSGSYNPNNGNSYISVTGMSRNPLEIYIYENFGTYNPGATKLGVTCDGSVYDIYRT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 NFSGSYNPNNGNSYISVTGMSRNPLEIYIYENFGTYNPGATKLGVTSDGSVYDIYRT 120

QY 121 QRVNAPSIIEGTAFYQYWSVRNHRSSGSVNTACHFNAMAQHGILTLGTMVQIVAVEGYF 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 QRVNAPSIIEGTAFYQYWSVRNHRSSGSVNTANHFNAMAQHGILTLGTMVQIVAVEGYF 180

QY 181 SSGSASITVS 190
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 SSGSASITVS 190
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Search completed: June 30, 2004, 19:39:28
Job time : 48.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:36:09 ; Search time 14 Seconds

(without alignments)
700.638 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054

Sequence: 1 QRIQPTGNGYFYSYVND.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/iaa/6C_COMB.pep:*
6: /cgn2_6/prodata/2/iaa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	190	1	US-08-044-621D-26
2	986	93.5	190	1	US-08-709-912-16
3	986	93.5	190	2	US-09-047-370-16
4	986	93.5	223	2	US-08-121-435A-2
5	985	93.5	223	3	US-09-254-733-7
6	981	93.1	190	4	US-09-570-856B-22
7	976	92.6	190	2	US-08-709-912-17
8	976	92.6	190	2	US-09-047-370-17
9	973	92.3	190	1	US-08-044-621D-27
10	963	91.4	190	4	US-09-570-856B-19
11	953	90.4	190	1	US-08-044-621D-28
12	953	90.4	190	1	US-08-709-912-14
13	953	90.4	190	2	US-09-047-370-14
14	947	89.8	190	4	US-09-570-856B-20
15	728.5	69.1	261	4	US-08-768-373-2
16	728.5	69.1	261	4	US-09-849-242A-2
17	651.5	61.8	225	2	US-08-886-765-2
18	651.5	61.8	225	3	US-09-115-660-2
19	646.5	61.3	194	4	US-09-570-856B-24
20	646.5	61.3	194	4	US-09-570-856B-26
21	639.5	60.7	194	4	US-09-570-856B-23
22	638.5	60.6	230	3	US-08-768-373-4
23	638.5	60.6	230	4	US-09-849-242A-4
24	633.5	60.1	225	1	US-08-290-979A-8
25	632.5	60.0	189	1	US-08-709-912-13
26	632.5	60.0	189	2	US-09-047-370-13
27	626.5	59.4	221	4	US-09-570-856B-29

28	617.5	58.6	223	4	US-09-462-246-2	Sequence 2, Appli
29	608	57.7	226	4	US-09-367-891A-2	Sequence 2, Appli
30	602.5	57.2	344	2	US-08-468-812-2	Sequence 2, Appli
31	602.5	57.2	344	4	US-08-590-563-2	Sequence 2, Appli
32	602.5	57.2	344	4	US-09-770-621-2	Sequence 2, Appli
33	602.5	57.2	344	4	US-09-235-832-2	Sequence 2, Appli
34	601.5	57.1	227	1	US-08-458-023B-4	Sequence 4, Appli
35	601	57.0	231	2	US-08-902-655A-6	Sequence 6, Appli
36	601	57.0	236	1	US-08-507-431-6	Sequence 6, Appli
37	601	57.0	296	3	US-09-116-622-6	Sequence 6, Appli
38	601	57.0	296	3	US-09-219-277-6	Sequence 6, Appli
39	582	55.2	206	1	US-09-599-661-6	Sequence 6, Appli
40	582	55.2	206	1	US-08-315-695-19	Sequence 6, Appli
41	582	55.2	215	1	US-08-044-621D-34	Sequence 34, Appli
42	582	55.2	335	4	US-09-570-856B-15	Sequence 15, Appli
43	580	55.0	191	1	US-08-709-912-10	Sequence 10, Appli
44	580	55.0	191	2	US-09-047-370-10	Sequence 10, Appli
45	572.5	54.3	197	1	US-08-044-621D-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1
US-08-044-621D-26
Sequence 26, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wing L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XILANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESS: Gowling, Strachy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1G3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Stratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDEDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: No
HYPOTHETICAL: No
ANTI-SENSE: No

FRAGMENT TYPE: NO
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Trichoderma reesei, XYN II, 21kD, pi 9.0
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Torronene, A., Mach, R.L., Messner, R.,
AUTHORS: Gonzalez, R., Kalkinen, N., Harkki, A.,
AUTHORS: & Kubicek, C.P.
TITLE:
JOURNAL: Bio/Technology
VOLUME: 10
ISSUE:
PAGES: 1461-1465
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-26

Query Match 93.5%; Score 986; DB 1; Length 190;
Best Local Similarity 95.3%; Pred. No. 6.8e-85;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYGYMNDHGCVMTLPGGQFVYVNSGDFVAGKMGQPTKXKVI 60
DB 1 QTIQPGTGHNGYFYGYMNDHGCVMTLPGGQFVYVNSGDFVAGKMGQPTKXKVI 60
QY 61 NFGSYVNGNSYLSVYGWNRNPLIEYIYVENFGTYPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFGSYVNGNSYLSVYGWNRNPLIEYIYVENFGTYPSTGATKLGCVTCDGSVYDIYRT 120
QY 121 QRVNAPSIETATFYQYWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIVAVGXYF 180
DB 121 QRVNAPSIETATFYQYWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIVAVGXYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 2

US-08-709-912-16
Sequence 16, Application US/08709912
Patent No. 575840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Messner, R.
AUTHORS: Gonzalez, R
AUTHORS: Kalkinen, N
AUTHORS: Harkki, A
AUTHORS: Kubicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992

US-08-709-912-16
Query Match 93.5%; Score 986; DB 1; Length 190;
Best Local Similarity 95.3%; Pred. No. 6.8e-85;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYGYMNDHGCVMTLPGGQFVYVNSGDFVAGKMGQPTKXKVI 60
DB 1 QTIQPGTGHNGYFYGYMNDHGCVMTLPGGQFVYVNSGDFVAGKMGQPTKXKVI 60
QY 61 NFGSYVNGNSYLSVYGWNRNPLIEYIYVENFGTYPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFGSYVNGNSYLSVYGWNRNPLIEYIYVENFGTYPSTGATKLGCVTCDGSVYDIYRT 120
QY 121 QRVNAPSIETATFYQYWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIVAVGXYF 180
DB 121 QRVNAPSIETATFYQYWSVRNRHSSGSVNTACHENMAQOGLTGTMDYQIVAVGXYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3

US-09-047-370-16
Sequence 16, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: Internal
ORGANISM: Trichoderma reesei
STRAIN: Xyn II
PUBLICATION INFORMATION:
AUTHORS: Torronene, A
AUTHORS: Mach, R. L.
AUTHORS: Mesner, R
AUTHORS: Gonzalez, R
AUTHORS: Kalkinen, N
AUTHORS: Hakki, A
AUTHORS: Kudicek, C. P.
JOURNAL: Biotechnology
VOLUME: 10
PAGES: 1461-1465
DATE: 1992
US-09-047-370-16

Query Match 93.5%; Score 986; DB 2; Length 190;
Best Local Similarity 95.3%; Pred. No. 6.8e-85;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTLPQGTGNGYFYSYVWNGHGVYMTLPGGQFVWNSGDFVGGKMGPGTKNKVI 60
DB 1 QTLPQGTGNGYFYSYVWNGHGVYMTLPGGQFVWNSGDFVGGKMGPGTKNKVI 60
QY 61 NFGSGYVNPNGSYLSVYGMGRNPLIEYIVENFGTVNPGTATKGEVTCDSYVDIYRT 120
DB 61 NFGSGYVNPNGSYLSVYGMGRNPLIEYIVENFGTVNPGTATKGEVTCDSYVDIYRT 120
QY 121 QRVNAPEIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNAPEIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 4
US-08-121-436A-2
Sequence 2, Application US/08121436A
Patent No. 5837515
GENERAL INFORMATION:
APPLICANT: Suominen, Pirkko

APPLICANT: Nevalainen, Helena
APPLICANT: Saarelainen, Riitta
APPLICANT: Paloheimo, Marja
APPLICANT: Lehtinen, Tarja
APPLICANT: Fagerström, Richard
TITLE OF INVENTION: No. 5837515el Enzyme Preparations and Methods
TITLE OF INVENTION: for Their Production
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stearne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,436A
FILING DATE: 16-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,478
FILING DATE: 18-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FI93/00221
FILING DATE: 24-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,893
FILING DATE: 29-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/524,308
FILING DATE: 16-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.008000C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 223 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-436A-2

Query Match 93.5%; Score 986; DB 2; Length 223;
Best Local Similarity 95.3%; Pred. No. 8.4e-85;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTLPQGTGNGYFYSYVWNGHGVYMTLPGGQFVWNSGDFVGGKMGPGTKNKVI 60
DB 34 QTLPQGTGNGYFYSYVWNGHGVYMTLPGGQFVWNSGDFVGGKMGPGTKNKVI 93
QY 61 NFGSGYVNPNGSYLSVYGMGRNPLIEYIVENFGTVNPGTATKGEVTCDSYVDIYRT 120
DB 61 NFGSGYVNPNGSYLSVYGMGRNPLIEYIVENFGTVNPGTATKGEVTCDSYVDIYRT 120
QY 121 QRVNAPEIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNAPEIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAQGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 223

RESULT 5
US-09-254-733-7

```

; Sequence 7, Application US/09254733
; Patent No. 6277596
; GENERAL INFORMATION:
; APPLICANT: MATANABE, MANABU
; APPLICANT: MORIYA, TATSUKI
; APPLICANT: AOYAGI, KAORI
; APPLICANT: SUMIDA, NAOMI
; APPLICANT: MURAKAMI, TAKESHI
; TITLE OF INVENTION: REGULATORY SEQUENCE OF CELLULOSE CBH1 GENES ORIGINATING
; TITLE OF INVENTION: IN TRICHODERMA VIRIDE AND SYSTEM FOR MASS-PRODUCING
; FILE REFERENCE: 99-0266*/LC(MMC)/00144
; CURRENT APPLICATION NUMBER: US/09/254,733
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 223
; TYPE: PRT
; ORGANISM: TRICHODERMA VIRIDE MC300-1
US-09-254-733-7

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Query Match          93.5%; Score 985; DB 3; Length 223;
Best Local Similarity 94.2%; Pred. No. 1e-84;
Matches 179; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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QY 1 OTTQPGTGYHNGYFYSYWMDHGCVMTLGGPGGFSVWNSGDFVGGKMGQPGTKNKYI 60
DB 34 OTTQPGTGYHNGYFYSYWMDHGCVMTLGGPGGFSVWNSGDFVGGKMGQPGTKNKYI 93
QY 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIIVENFGYVNSTGATKLGCVTCDGSVYDIYRT 120
DB 94 NFSGTVPNGNSLSYVWGSRNPLIEYIIVENFGYVNSTGATKLGCVTSDGSVYDIYRT 153
QY 121 QRVNABIEGTATFYQVWSVRNRHRSRSGSVNTACHNMAQHGTLTGMDYQIVAVEGYF 180
DB 154 QRVNABIEGTATFYQVWSVRNRHRSRSGSVNTACHNMAQHGTLTGMDYQIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGSASITVS 223

```

```

RESULT 6
US-09-570-856B-22
; Sequence 22, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzen, Joerg M
; APPLICANT: Dahiyat, Bassil I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RT/EMS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma reesei
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: "Xaa" at position 1 is non-std-residue "PCA NH3+"
US-09-570-856B-22

```

```

Query Match          93.1%; Score 981; DB 4; Length 190;
Best Local Similarity 95.2%; Pred. No. 2e-84;
Matches 180; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
QY 2 TTQPGTGYHNGYFYSYWMDHGCVMTLGGPGGFSVWNSGDFVGGKMGQPGTKNKYIN 61

```

```

DB 2 TTQPGTGYHNGYFYSYWMDHGCVMTLGGPGGFSVWNSGDFVGGKMGQPGTKNKYIN 61
QY 62 FSGSYNPNNGSYLSYVWGSRNPLIEYIIVENFGYVNSTGATKLGCVTCDGSVYDIYRTQ 121
DB 62 FSGSYNPNNGSYLSYVWGSRNPLIEYIIVENFGYVNSTGATKLGCVTSDGSVYDIYRTQ 121
QY 122 RVNAPSIIGTATFYQVWSVRNRHRSRSGSVNTACHNMAQHGTLTGMDYQIVAVEGYF 181
DB 122 RVNAPSIIGTATFYQVWSVRNRHRSRSGSVNTACHNMAQHGTLTGMDYQIVAVEGYF 181
QY 182 SSGSASITVS 190
DB 182 SSGSASITVS 190

```

```

RESULT 7
US-08-709-912-17
; Sequence 17, Application US/08709912
; Patent No. 5759640
; GENERAL INFORMATION:
; APPLICANT: Sung Dr., Wing L
; APPLICANT: Yaguchi Dr., Makoto
; APPLICANT: Ishikawa Dr., Kazuhiko
; TITLE OF INVENTION: Modification of Xylanase to Improve
; TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fitzpatrick, Cella, Harper, and Scinto
; STREET: 277 Park Ave.
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10172-0194
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,912
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen M, Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1039.2000
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma viride
; PUBLICATION INFORMATION:
; AUTHORS: Yaguchi, M
; AUTHORS: Roy, C
; AUTHORS: Ujie, M
; AUTHORS: Watson, D. C.
; AUTHORS: Makarchuk, W.
; JOURNAL: Xylan and Xylanase
; PAGES: 149-154
; DATE: 1992
US-08-709-912-17

```

Query Match 92.6%; Score 976; DB 1; Length 190;
Best Local Similarity 94.2%; Pred. No. 5.9e-84;
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYSYVNDGSGVTMLGPGGQPSVWMSNSGDPVGGKMGQPGTKNXYI 60
DB 1 QTIQPGYHNGYFYSYVNDGSGVTMLGPGGQPSVWMSNSGDPVGGKMGQPGTKNXYI 60
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIYVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIYVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
QY 121 QRYNAPSIETGATFYQYWSVRNRRSSGSVNTACHFNMAQHGTLTGMDYQIYAVEGYF 180
DB 121 QRYNAPSIETGATFYQYWSVRNRRSSGSVNTAHFNMAQHGTLTGMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 8

US-09-047-370-17
Sequence 17, Application US/09047370
Patent No. 5866408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Ming L
APPLICANT: Yaguchi Dr., Makoto
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of xylanase to improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/047,370
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/709,912
FILING DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr., Warren B
REGISTRATION NUMBER: 27290
REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
PUBLICATION INFORMATION:

AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Ujle, M
AUTHORS: Watson, D. C.
AUTHORS: Makarchuk, W.
JOURNAL: Xylan and Xylanase
PAGES: 149-154
DATE: 1992
US-09-047-370-17

Query Match 92.6%; Score 976; DB 2; Length 190;
Best Local Similarity 94.2%; Pred. No. 5.9e-84;
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGYHNGYFYSYVNDGSGVTMLGPGGQPSVWMSNSGDPVGGKMGQPGTKNXYI 60
DB 1 QTIQPGYHNGYFYSYVNDGSGVTMLGPGGQPSVWMSNSGDPVGGKMGQPGTKNXYI 60
QY 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIYVENFGTYNPGTGATKLGVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGSYLSYVGMRSNPLIEYIYVENFGTYNPGTGATKLGVTSDGSVYDIYRT 120
QY 121 QRYNAPSIETGATFYQYWSVRNRRSSGSVNTACHFNMAQHGTLTGMDYQIYAVEGYF 180
DB 121 QRYNAPSIETGATFYQYWSVRNRRSSGSVNTAHFNMAQHGTLTGMDYQIYAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 9

US-08-044-621D-27
Sequence 27, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Makarchuk
APPLICANT: Ming L. Sung
APPLICANT: Makoto Yaguchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowing, Strathy & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1G3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Eriact
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-766-0199
TELEFAX: 613-563-9869
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:

LENGTH: 190
TYPE: Amino Acid
STRANDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:
ORGANISM: Trichoderma viride
STRAIN: Trichoderma viride, 20KD
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yasuchi M., Roy C., Ujile M., Watson
AUTHORS: D.C., & Wakarchuk W.
TITLE: Amino Acid Sequence of the Low-Molecular-
weight Xylanase from Trichoderma viride
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 149-154
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-27

Query Match 92.3%; Score 973; DB 1; Length 190;
Best Local Similarity 93.7%; Pred. No. 1,1e-83;
Matches 178; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTPTGTHNGYFYSYNDHGHGVTMTLGPQGQPSYVNSGDPFVGKGMQPGTKNKVI 60
DB 1 OTTPTGTHNGYFYSYNDHGHGVTMTLGPQGQPSYVNSGDPFVGKGMQPGTKNKVI 60
QY 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
QY 121 QRVNAPSIEGTATFYQVYSVRNRHSSGSVNTACHFNAMAGHLTLGTMDOYQIVAVEGYF 180
DB 121 QRVNAPSIEGTATFYQVYSVRNRHSSGSVNTACHFNAMAGHLTLGTMDOYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 10
US-09-570-856B-19
Sequence 19, Application US/09570856B
Patent No. 6682923
GENERAL INFORMATION:
APPLICANT: Benzihen, Joerg M
APPLICANT: Dahivat, Bassil I
TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
FILE REFERENCE: A-67478-1/RFT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/570, 856B
CURRENT FILING DATE: 2002-04-15
PRIOR APPLICATION NUMBER: US 60/133,714
PRIOR FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 19
LENGTH: 190
TYPE: PRT
ORGANISM: Trichoderma viride
US-09-570-856B-19

Query Match 91.4%; Score 963; DB 4; Length 190;
Best Local Similarity 92.6%; Pred. No. 9,8e-83;
Matches 176; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 OTTPTGTHNGYFYSYNDHGHGVTMTLGPQGQPSYVNSGDPFVGKGMQPGTKNKVI 60
DB 1 OTTPTGTHNGYFYSYNDHGHGVTMTLGPQGQPSYVNSGDPFVGKGMQPGTKNKVI 60
QY 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
DB 61 NFSGTYNPNNGNSYLSVYGMRSNPLIEYIVENFGTYNPSTGATKLGCVTSDGSVDIYRT 120
QY 121 QRVNAPSIEGTATFYQVYSVRNRHSSGSVNTACHFNAMAGHLTLGTMDOYQIVAVEGYF 180
DB 121 QRVNAPSIEGTATFYQVYSVRNRHSSGSVNTACHFNAMAGHLTLGTMDOYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 11
US-08-044-621D-28
Sequence 28, Application US/08044621D
Patent No. 5405769
GENERAL INFORMATION:
APPLICANT: Warren W. Wakarchuk
APPLICANT: Wang L. Sung
APPLICANT: Makoto Yasuchi
APPLICANT: Robert L. Campbell
APPLICANT: David R. Rose
TITLE OF INVENTION: CONSTRUCTION OF THERMOSTABLE MUTANTS
TITLE OF INVENTION: OF A LOW MOLECULAR MASS XYLANASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gowing, Strathly & Henderson
STREET: Suite 2600, 160 Elgin Street
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1P 1C3
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 in., 360KB storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/044,621D
FILING DATE: April 8, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Judy A. Erratt
REGISTRATION NUMBER: 34,076
REFERENCE/DOCKET NUMBER: 08-863796
TELECOMMUNICATION INFORMATION:
TELEPHONE: 613-786-0199
TELEFAX: 613-563-9869
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 190
TYPE: Amino Acid
STRANDNESS: No. 5405769 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No
ORIGINAL SOURCE:

ORGANISM: Trichoderma harzianum
STRAIN: Trichoderma harzianum, 20kd
IMMEDIATE SOURCE:
POSITION IN GENOME:
FEATURE:
PUBLICATION INFORMATION:
AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
AUTHORS: F., Tan L.U.L., Senior D.U., & Saddler
AUTHORS: J.N.
TITLE:
JOURNAL: Xylans and Xylanases
VOLUME:
ISSUE:
PAGES: 435-438
DATE: 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-044-621D-28

Query Match 90.4%; Score 953; DB 1; Length 190;
Best Local Similarity 91.6%; Pred. No. 8.5e-82;
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIGPGTGHNGYFYSYVNDGAGVTMTLGGGQPSVWMSNGDFVGGKMGQPGTKNXYI 60
DB 1 QTIGPGTGHNGYFYSYVNDGAGVTMTLGGGQPSVWMSNGDFVGGKMGQPGTKNXYI 60

QY 61 NFSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGYNPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGYNPSTGATKLGCVTSDGSVYDIYRT 120

QY 121 QRNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180
DB 121 QRNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 12
US-08-709-912-14
Sequence 14, Application US/08709912
Patent No. 5759840
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Ishikawa Dr., Makoto
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,912
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Olsen Mr, Warren E
REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-2400
TELEFAX: (212) 758-2982
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 190 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Trichoderma harzianum
PUBLICATION INFORMATION:
AUTHORS: Yaguchi, M
AUTHORS: Roy, C
AUTHORS: Watson, D. C.
AUTHORS: Rollin, F
AUTHORS: Tan, L. U. L.
AUTHORS: Senior, D. U.
AUTHORS: Saddler, J. N.
JOURNAL: Xylan and Xylanase
PAGES: 435-438
DATE: 1992
US-08-709-912-14

Query Match 90.4%; Score 953; DB 1; Length 190;
Best Local Similarity 91.6%; Pred. No. 8.5e-82;
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIGPGTGHNGYFYSYVNDGAGVTMTLGGGQPSVWMSNGDFVGGKMGQPGTKNXYI 60
DB 1 QTIGPGTGHNGYFYSYVNDGAGVTMTLGGGQPSVWMSNGDFVGGKMGQPGTKNXYI 60

QY 61 NFSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGYNPSTGATKLGCVTCDGSVYDIYRT 120
DB 61 NFSGSYNPNNGNSYLSVYGSRNPLIEYIVENFGYNPSTGATKLGCVTSDGSVYDIYRT 120

QY 121 QRNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180
DB 121 QRNAPSIIEGTATFYQYWSVRNRHSSGSVNTACHFNMAAOGHGLTGMDYQIVAVEGYF 180

QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 13
US-09-047-370-14
Sequence 14, Application US/09047370
Patent No. 5666408
GENERAL INFORMATION:
APPLICANT: Sung Dr., Wing L
APPLICANT: Ishikawa Dr., Kazuhiko
TITLE OF INVENTION: Modification of Xylanase to Improve
TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
TITLE OF INVENTION: Thermostability
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
STREET: 277 Park Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/047,370
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/709,912
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Olsen Mr. Warren E
; REGISTRATION NUMBER: 27290
; REFERENCE/DOCKET NUMBER: 1035.2000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-2400
; TELEFAX: (212) 758-2982
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Trichoderma harzianum
; PUBLICATION INFORMATION:
; AUTHORS: Yaquchi, M
; AUTHORS: Roy, C
; AUTHORS: Mateon, D. C.
; AUTHORS: Rollin, P.
; AUTHORS: Tan, L. U. L.
; AUTHORS: Senior, D. J.
; AUTHORS: Saddler, J. N.
; JOURNAL: Xylan and Xylanase
; PAGES: 435-438
; DATE: 1992
;
US-09-047-370-14
;
Query Match 90.4%; Score 953; DB 2; Length 190;
Best Local Similarity 91.6%; Pred. No. 8.5e-82;
Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
;
QY 1 QTIQPGTGYNGYFYSWNDGSGVMTLPQGPFSVNMNSGDFVCGKMGPGTKNKVI 60
DB 1 QTIQPGTGYNSGYYSWMDGAGVITYNCGGGSFTVNMNSGDFVCGKMGPGTKNKVI 60
QY 61 NFGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
DB 61 NFGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
QY 121 QRVNAPSEIETATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180
DB 121 QRVNAPSEIETATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180
QY 181 SSGSASTIVS 190
DB 181 SSGSASTIVS 190
;
RESULT 14
US-09-570-856B-20
; Sequence 20, Application US/09570856B
; Patent No. 6682923
; GENERAL INFORMATION:
; APPLICANT: Bentzien, Joerg M
; APPLICANT: Dahiyat, Basill I
; TITLE OF INVENTION: NOVEL THERMOSTABLE ALKALIPHILIC XYLANASE
; FILE REFERENCE: A-67478-1/RFT/MS/RMK
; CURRENT APPLICATION NUMBER: US/09/570,856B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/133,714

```

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; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-09-570-856B-20
;
Query Match 89.8%; Score 947; DB 4; Length 190;
Best Local Similarity 91.1%; Pred. No. 3.1e-81;
Matches 173; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
;
QY 1 QTIQPGTGYNGYFYSWNDGSGVMTLPQGPFSVNMNSGDFVCGKMGPGTKNKVI 60
DB 1 QTIQPGTGYNSGYYSWMDGAGVITYNCGGGSFTVNMNSGDFVCGKMGPGTKNKVI 60
QY 61 NFGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
DB 61 NFGSYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
QY 121 QRVNAPSEIETATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180
DB 121 QRVNAPSEIETATFYQVWSVRNRHSSGSVNTACHFNAMAQHGILLGTMDYQIVAVEGYF 180
QY 181 SSGSASTIVS 190
DB 181 SSGSASTIVS 190
;
RESULT 15
US-08-768-373-2
; Sequence 2, Application US/08768373
; Patent No. 6228629
; GENERAL INFORMATION:
; APPLICANT: PALOHEIMO, MARJA
; APPLICANT: HAKOLA, SATU
; APPLICANT: M NTYL, ARJA
; APPLICANT: VEHMAANPER, JARI
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: LAHTINEN, TARJA
; APPLICANT: FAGERSTEN, M. RICHARD
; APPLICANT: SUOMINEN, PIIRKO
; TITLE OF INVENTION: NOVEL XYLANASES, GENES ENCODING THEM,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/768,373
; FILING DATE: 17-DEC-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,746
; FILING DATE: 18-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,839
; FILING DATE: 28-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CIMBALA, MICHELE A.
; REGISTRATION NUMBER: 33,851
; REFERENCE/DOCKET NUMBER: 1050.0540003
; TELECOMMUNICATION INFORMATION:

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TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Chaetomium thermophilum
STRAIN: CBS730.95
FEATURE:
NAME/KEY: Protein
LOCATION: 1..261
OTHER INFORMATION: /label= X1NA
US-08-768-373-2

Query Match .69.1%; Score 728.5; DB 3; length 261;
Best Local Similarity 66.8%; Pred. No. 1.4e-60;
Matches 127; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY	1	QTI-QPCTGHNQYFYSYVNDGHSVTMTLGPCCQFSVNMNSGDFVGGKMQPCTKNKY	59
DB	27	QTLTSSATGHNQYYSFWTDGQGNIRFNLESQGYSVTWSGNGWVGKGNPCTDNRY	86
QY	60	INPSGSYNPQNSYLSVYSGSRNPLIEYIVENFGTYNPSTGATKLGKGEVTCDSVYDIYR	119
DB	87	INTADYRPNQNSYLAVGNTNPLIEYIVESFGTYDSTGATKRGSVTTDGGTYNIR	146
QY	120	TQRVNAPSIEGATFYQYWSVRNRHSSGGSVNTACHFNMAAQHGLTLGTMVQIVAVEGY	179
DB	147	TQRVNAPSIEGATFYQYWEVTRTSKRTGCTVTMANHFNMRQAGLQGSMDYQIVAVEGY	206
QY	180	FSSGSASITY	189
DB	207	YSSGSATVNV	216

Search completed: June 30, 2004, 19:44:48
Job time : 14 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:40:15 ; Search time 37.25 Seconds

(without alignments)
1441.987 Million cell updates/sec

Title: US-09-856-025b-65

Perfect score: 1054 1 QTIQPTGYHNGYFYSYWMD.....YQIVAVEGYFSSGSASITVS 190

Sequence: 1 QTIQPTGYHNGYFYSYWMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1166195 segs, 282705291 residues

Total number of hits satisfying chosen parameters: 1166195

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep:*
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11: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep:*
15: /cgn2_6/prodata/2/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	190	US-10-307-441-16	Sequence 16, Appl
2	986	93.5	222	US-10-237-386-32	Sequence 32, Appl
3	986	93.5	223	US-10-237-386-31	Sequence 31, Appl
4	976	92.6	190	US-10-307-441-17	Sequence 17, Appl
5	974	92.4	223	US-10-237-386-30	Sequence 30, Appl
6	953	90.4	190	US-10-307-441-14	Sequence 14, Appl
7	947	89.8	190	US-10-237-386-33	Sequence 33, Appl
8	829	78.7	223	US-10-237-386-34	Sequence 34, Appl
9	739.5	70.2	241	US-10-237-386-35	Sequence 35, Appl
10	678.5	64.4	219	US-10-237-386-29	Sequence 29, Appl
11	660.5	62.7	227	US-10-237-386-22	Sequence 22, Appl
12	654.5	62.1	227	US-10-237-386-21	Sequence 21, Appl
13	651.5	61.8	194	US-10-307-441-20	Sequence 20, Appl
14	651.5	61.8	225	US-09-467-368-2	Sequence 2, Appl
15	651.5	61.8	225	US-10-237-386-24	Sequence 24, Appl

16	649.5	61.6	234	US-10-213-990-69	Sequence 69, Appl
17	642	60.9	313	US-10-213-990-72	Sequence 72, Appl
18	639.5	60.7	189	US-10-307-441-19	Sequence 19, Appl
19	637.5	60.5	221	US-10-213-990-66	Sequence 66, Appl
20	632.5	60.0	189	US-10-307-441-13	Sequence 13, Appl
21	632.5	60.0	225	US-10-237-386-36	Sequence 36, Appl
22	632.5	60.0	240	US-10-237-386-42	Sequence 42, Appl
23	626.5	59.4	221	US-10-237-386-40	Sequence 40, Appl
24	624.5	59.3	231	US-10-237-386-26	Sequence 26, Appl
25	623.5	59.2	239	US-10-237-386-40	Sequence 40, Appl
26	621.5	59.0	241	US-10-237-386-37	Sequence 37, Appl
27	620	58.8	221	US-10-237-386-37	Sequence 37, Appl
28	617.5	58.6	223	US-10-237-386-25	Sequence 25, Appl
29	617.5	58.6	231	US-10-237-386-25	Sequence 25, Appl
30	603	57.2	228	US-10-237-386-39	Sequence 39, Appl
31	602.5	57.2	344	US-09-770-621-2	Sequence 2, Appl
32	602.5	57.2	344	US-10-286-993-2	Sequence 2, Appl
33	600.5	57.0	221	US-10-237-386-44	Sequence 44, Appl
34	598	56.7	217	US-09-790-070A-11	Sequence 11, Appl
35	595.5	56.5	227	US-10-237-386-27	Sequence 27, Appl
36	594.5	56.4	242	US-10-237-386-41	Sequence 41, Appl
37	580	55.0	191	US-10-307-441-10	Sequence 10, Appl
38	572.5	54.3	197	US-10-307-441-9	Sequence 9, Appl
39	572.5	54.3	201	US-10-237-386-23	Sequence 23, Appl
40	572	54.3	216	US-10-237-386-45	Sequence 45, Appl
41	552.5	52.4	233	US-10-237-386-28	Sequence 28, Appl
42	534.5	50.7	226	US-10-237-386-63	Sequence 63, Appl
43	533.5	50.6	189	US-10-307-441-12	Sequence 12, Appl
44	531	50.4	191	US-10-307-441-11	Sequence 11, Appl
45	531	50.4	240	US-10-237-386-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-307-441-16
; Sequence 16, Application US/10307441
; Publication No. US20030166236A1
GENERAL INFORMATION:
; APPLICANT: SONG, Ming L.
; TITLE OF INVENTION: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 02767-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-307-441-16

Query Match 93.5%; Score 986; DB 14; Length 190;
Best Local Similarity 95.3%; Pred. No. 5.5e-90;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPTGYHNGYFYSYWMDHGQVMTLTPGPGGGSVWMSNGDFVGKGMQPGTKNKVY 60
DB 61 NFGSGNPNKGNLYLVYSGSRNPLLEYIVTFVFGYNSGTGATKCEYTCGQSVYDIKT 120
QY 61 NFGSGNPNKGNLYLVYSGSRNPLLEYIVTFVFGYNSGTGATKCEYTCGQSVYDIKT 120
DB 61 NFGSGNPNKGNLYLVYSGSRNPLLEYIVTFVFGYNSGTGATKCEYTCGQSVYDIKT 120
QY 121 QRVNAPSIKGIATFYQYWSVRNHRSSGSVNTACHFNMAQHGTLTGTDYQIVAVEGYF 180

Db 121 QRVNPSIIIGTATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

RESULT 2
US-10-237-386-32

; Sequence 32, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 222
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-32

Query Match 93.5%; Score 986; DB 14; Length 222;
Best Local Similarity 95.3%; Pred. No. 6.6e-90;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 60
Db 33 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 92
QY 61 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTCDGSYYDIYRT 120
Db 93 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTSDGSYYDIYRT 152
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTMDOYIVAVEGYF 180
Db 153 QRVNAPSIIIGTATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTMDOYIVAVEGYF 212
QY 181 SSGSASITVS 190
Db 213 SSGSASITVS 222

RESULT 3

US-10-237-386-31
; Sequence 31, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sorensen, Ole
; APPLICANT: Sorensen, Ole
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-31

Query Match 93.5%; Score 986; DB 14; Length 223;
Best Local Similarity 95.3%; Pred. No. 6.7e-90;
Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 60
Db 34 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 93
QY 61 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTCDGSYYDIYRT 120
Db 94 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTSDGSYYDIYRT 153
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTMDOYIVAVEGYF 180
Db 154 QRVNAPSIIIGTATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTMDOYIVAVEGYF 213
QY 181 SSGSASITVS 190
Db 214 SSGSASITVS 223

RESULT 4

US-10-307-441-17
; Sequence 17, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wang L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma viride
US-10-307-441-17

Query Match 92.6%; Score 976; DB 14; Length 190;
Best Local Similarity 94.2%; Pred. No. 5.4e-89;
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 60
Db 1 QTIQPGTGYHNGYFYSYNNDDHGGVMTLGGGQFVSVMWSNGDFVGGKMGQPGTKNKVI 60
QY 61 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTCDGSYYDIYRT 120
Db 61 NFSGSYNPNNGSYLSVYSGMSRNPILIEYIVENFGTNPSTGATYKLGVTSDGSYYDIYRT 120
QY 121 QRVNAPSIEGATFYQYMSVRRNRSSGSVNTACHFNAMAQOGLTLGTMDOYIVAVEGYF 180
Db 121 QRVNAPSIIIGTATFYQYMSVRRNRSSGSVNTANHFNAQAQGLTLGTMDOYIVAVEGYF 180
QY 181 SSGSASITVS 190
Db 181 SSGSASITVS 190

```

RESULT 5
US-10-237-386-30
; Sequence 30, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 223
; TYPE: PRT
; ORGANISM: T. reesei
US-10-237-386-30

Query Match          92.4%; Score 574; DB 14; Length 223;
Best Local Similarity 94.2%; Pred. No. 1e-88;
Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 60
   |||||
DB 34 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 93
   |||||

QY 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
   |||||
DB 94 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 153
   |||||

QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 180
   |||||
DB 154 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 213
   |||||

QY 181 SSGSASITVS 190
   |||||
DB 214 SSGSASITVS 223
   |||||

RESULT 6
US-10-307-441-14
; Sequence 14, Application US/10307441
; Publication No. US20030166236A1
; GENERAL INFORMATION:
; APPLICANT: SUNG, Wing L.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
; FILE REFERENCE: 027367-5006US
; CURRENT APPLICATION NUMBER: US/10/307,441
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: PCT/CA01/00769
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/213,803
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Trichoderma harzianum
US-10-307-441-14

Query Match          90.4%; Score 953; DB 14; Length 190;
Best Local Similarity 91.6%; Pred. No. 1.1e-86;

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Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 60
   |||||
DB 1 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 60
   |||||

QY 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
   |||||
DB 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
   |||||

QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 180
   |||||
DB 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 180
   |||||

QY 181 SSGSASITVS 190
   |||||
DB 181 SSGSASITVS 190
   |||||

RESULT 7
US-10-237-386-33
; Sequence 33, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole
; APPLICANT: Sorensen, Jens
; TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
; FILE REFERENCE: 674509-2046
; CURRENT APPLICATION NUMBER: US/10/237,386
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: PCT/IB01/00426
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: GB 0005585.5
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: GB 0015751.1
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 190
; TYPE: PRT
; ORGANISM: T. harzianum
US-10-237-386-33

Query Match          89.8%; Score 947; DB 14; Length 190;
Best Local Similarity 91.1%; Pred. No. 4.2e-86;
Matches 173; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 60
   |||||
DB 1 OTTQPGYHNGYFYSYWNDDGHGVTMTLGPQGQFVSVMNSGDFVGGKMGQPGTKNKYI 60
   |||||

QY 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
   |||||
DB 61 NFSGSYNPNNGSYLSYVWGSRNPLIEYIVENFGTYNPGTATKLGVTCDGSVYDIYRT 120
   |||||

QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 180
   |||||
DB 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHLGLTGMTDYOIVAVEGYF 180
   |||||

QY 181 SSGSASITVS 190
   |||||
DB 181 SSGSASITVS 190
   |||||

RESULT 8
US-10-237-386-34
; Sequence 34, Application US/10237386
; Publication No. US20030180895A1
; GENERAL INFORMATION:
; APPLICANT: Danisco A/S
; APPLICANT: Sibiessen, Ole

```

APPLICANT: Sorensen, Jens
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 223
TYPE: PRT
ORGANISM: T. viride
US-10-237-386-34

Query Match 78.7%; Score 829; DB 14; Length 223;
Best Local Similarity 78.4%; Pred. No. 2,5e-74;
Matches 149; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 OTTQPGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYI 60
DB 34 OTTQPGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYI 93
QY 61 NFGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRT 120
DB 94 NFGSYNPNNGNSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRT 153
QY 121 QRVNAPSEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYF 180
DB 154 QRVNAPSEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYF 213
QY 181 SSGSASITVS 190
DB 214 SSGNANITVS 223

RESULT 9
US-10-237-386-35
Sequence 35, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 241
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-35

Query Match 70.2%; Score 739.5; DB 14; Length 241;
Best Local Similarity 71.6%; Pred. No. 2,5e-65;
Matches 131; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYINFSGSY 66
DB 38 TGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYINFSGSY 96

QY 67 NPNNGSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRTQVNAP 126
DB 97 NPNNGSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRTQVNAP 156
QY 127 SIEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYFSSGSAS 186
DB 157 SIEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYFSSGSAS 216
QY 187 ITV 189
DB 217 VNV 219

RESULT 10
US-10-237-386-29
Sequence 29, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: PCT/IB01/00426
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: GB 0005585.5
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: GB 0015751.1
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 219
TYPE: PRT
ORGANISM: C. gracile
US-10-237-386-29

Query Match 64.4%; Score 678.5; DB 14; Length 219;
Best Local Similarity 65.9%; Pred. No. 2,6e-59;
Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYINFSGS 65
DB 36 GTGYHNGYFYSYNDGSGVTMTLGPQGFVSVMNSGDFVGGKQWPGTKNKYINFSGS 94
QY 66 YNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRTQVNA 125
DB 95 YNPNNGSYLSVYGMSRNPILIEYIVENFGTYNPSTGATKLGVTCDGVDIYRTQVNA 154
QY 126 SIEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYFSSGSAS 185
DB 155 SIEGTATFYQWVSRNRHRSRGSVNTACHFNAMQHGLTGTMDYOIVAVEGYFSSGSAS 214
QY 186 SITVS 190
DB 215 SITVS 219

RESULT 11
US-10-237-386-22
Sequence 22, Application US/10237386
Publication No. US20030180895A1
GENERAL INFORMATION:
APPLICANT: Danisco A/S
APPLICANT: Sorensen, Ole
TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
FILE REFERENCE: 674509-2046
CURRENT APPLICATION NUMBER: US/10/237,386
CURRENT FILING DATE: 2002-12-06

PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 22
 LENGTH: 227
 TYPE: PRT
 ORGANISM: A. pisi
 US-10-237-386-22

Query Match 62.7%; Score 660.5; DB 14; Length 227;
 Best Local Similarity 63.7%; Pred. No. 1.7e-57;
 Matches 123; Conservative 21; Mismatches 44; Indels 5; Gaps 2;

QY 2 TTOPGT---GVHNGYFYSYVNDHGVTMTLGPQGGPSVWMSNGDFVGGKMQPGTKN 57
 DB 34 TAPAGTPSSGCTHNGCFYSWTDGAQATYTNAGAGSYVWMTGKGNLVGGKMPGAA- 92
 QY 58 KVINFGSYVNDGNSYLSVYVMSNPLEYIYVENFGTYNPGTATKLGVTCDGSYVDI 117
 DB 93 RTIYSGTSPSGNSYLAIVGWTENPLEYIYVENFGTYDPSQATVKGSVTDAGSSYKI 152
 QY 118 YRTORVAPSTEGTATFYQVWSYVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVE 177
 DB 153 AQOTRTNOPSIDGTQITQOQVWSVRNKRSSGSVNMKTHFPAAMAKMKLQTHNYQIYAVE 212
 QY 178 GFSSGSASITVS 190
 DB 213 GFSSGSASQITVN 225

RESULT 12
 US-10-237-386-21
 Sequence 21, Application US/10237386
 Publication No. US20030180895A1
 GENERAL INFORMATION:
 APPLICANT: Danisco A/S
 APPLICANT: Sibiessen, Ole
 TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitor
 FILE REFERENCE: 674509-2046
 CURRENT APPLICATION NUMBER: US/10/237,386
 PRIOR FILING DATE: 2002-12-06
 PRIOR APPLICATION NUMBER: PCT/IB01/00426
 PRIOR FILING DATE: 2001-03-08
 PRIOR APPLICATION NUMBER: GB 0005585.5
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: GB 0015751.1
 PRIOR FILING DATE: 2000-06-27
 NUMBER OF SEQ ID NOS: 66
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 21
 LENGTH: 227
 TYPE: PRT
 ORGANISM: H. turcicum
 US-10-237-386-21

Query Match 62.1%; Score 654.5; DB 14; Length 227;
 Best Local Similarity 62.6%; Pred. No. 6.6e-57;
 Matches 119; Conservative 23; Mismatches 47; Indels 1; Gaps 1;
 QY 1 OTTOPGTGYNHNGYFYVNDHGVTMTLGPQGGPSVWMSNGDFVGGKMQPGTKNRYI 60
 DB 37 QSTPNREGTNGCFYVMSDGAQATYTNAGAGSYVSWGTGKGNLVGGKMPGTA-RTI 95
 QY 61 NFSGSYVNDGNSYLSVYVMSNPLEYIYVENFGTYNPGTATKLGVTCDGSYVDIYRT 120
 DB 96 TYSGQYNPNSYLAIVGWTENPLEYIYVENFGTYDPSQATVKGSVTDAGSSYKIAS 155

QY 121 QRVNAPSIEGTATFYQVWSYVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYE 180
 DB 156 TRTNQPSIDGTRTFQGYWSVRNKRSSGSVNMKTHFDANAQKMLQSHYQIYAVEGYE 215
 QY 181 SSGSASITVS 190
 DB 216 SSGSASITVN 225

RESULT 13
 US-10-307-441-20
 Sequence 20, Application US/10307441
 Publication No. US20030166236A1
 GENERAL INFORMATION:
 APPLICANT: SUNG, Wing L.
 APPLICANT: National Research Council of Canada
 TITLE OF INVENTION: Modified Xylanases Exhibiting Increased Thermophilicity
 FILE REFERENCE: 027367-5006US
 CURRENT APPLICATION NUMBER: US/10/307,441
 PRIOR FILING DATE: 2002-12-02
 PRIOR APPLICATION NUMBER: PCT/CA01/00769
 PRIOR FILING DATE: 2001-05-31
 PRIOR APPLICATION NUMBER: 60/213,803
 PRIOR FILING DATE: 2000-05-31
 NUMBER OF SEQ ID NOS: 51
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20
 LENGTH: 194
 TYPE: PRT
 ORGANISM: Thermomyces lanuginosus
 US-10-307-441-20

Query Match 61.8%; Score 651.5; DB 14; Length 194;
 Best Local Similarity 60.7%; Pred. No. 1.1e-56;
 Matches 116; Conservative 29; Mismatches 45; Indels 1; Gaps 1;

QY 1 OTTOPGTGYNHNGYFYVNDHGVTMTLGPQGGPSVWMSNGDFVGGKMQPGTKNRYI 60
 DB 1 OTTNSGEGHNDGYYSWMSDGAQATYTNLEGGTYEISWGQGNLVGGKMPGNABAI 60
 QY 61 NFSGSYVNDGNSYLSVYVMSNPLEYIYVENFGTYNPGTATKLGVTCDGSYVDIYRT 120
 DB 61 HREGYQGNNGNSYLAIVGWTENPLEYIYVENFGTYDPSGATIDLGTCGGSIRLCKT 120
 QY 121 QRVNAPSIEGTATFYQVWSYVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGY 179
 DB 121 TRVNPASIDGTQTFQGYWSVRNKRSSGSVNTACHFNAMAQGNLVNDHYQIYAVEGY 180
 QY 180 FSSGSASITVS 190
 DB 181 FSSGSARITVA 191

RESULT 14
 US-09-467-368-2
 Sequence 2, Application US/09467368
 Patent No. US20020160080A1
 GENERAL INFORMATION:
 APPLICANT: Hansen, Peter Kamp
 Hansen, Peter
 Mullertz, Anette
 Knap, Inge Helmer
 TITLE OF INVENTION: Animal Feed Additives
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: No. US20020160080A1o No. US20020160080A1disk of No. US200201600
 STREET: 405 Lexington Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10174
 COMPUTER READABLE FORM:

```

1 MEDIUM TYPE: Diskette
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: DOS
4 SOFTWARE: FastSD for Windows Version 2.0
5
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/09/467,368
8 FILING DATE: 21-Dec-1999
9 CLASSIFICATION: <Unknown>
10
11 PRIORITY APPLICATION DATA:
12 APPLICATION NUMBER: US/08/886,765
13 FILING DATE: 1-Jul-1997
14
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Landtits, Elias J
17 REGISTRATION NUMBER: 33,728
18 REFERENCE/DOCKET NUMBER: 4324.204-US
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 212-867-0123
21 TELEFAX: 212-878-9655
22
23 INFORMATION FOR SEQ ID NO: 2:
24
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 225 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: protein
30 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
31
32 US-09-467-368-2

```

	Query March Best Local Similarity Matches	61.8%; 60.7%; 116;	Score 651.5; Pred. No. 1.3e-56; 29;	DB 9; Indels 45;	Length 225; Gaps 1;
Qy	1 QTTGPGGHHGPGSYVYNDHGQVMTLGGGCGPVSVMNSNSGDPFGKRGKMGQGTGKXVT				60
Db	32 QTPNBEQHHDDGYYSWMSDGAQNTNINLEGQVTEISWBGQGLVGGKMMNGLNARAI				91
Qy	61 NFGSSGNPNNGNYSLAYSGWMSNELLKEXITVNPCTNPNPSCATLGGYPCDGSVNYIYT				120
Db	92 HFGGVYQPNNGNYSLAYIGMTNPLVETIYVENFGTIVDPSSAIDDLGVECDGSIIYKGT				151
Qy	121 QRYNAPSIGTATLFOYMSVRENHSSGSVNTACHFNNAAOHGITL-GTMDIYIVAVEGT				179
Db	152 TRNAPASIDGTQFPQGYSVKRODKRTGTIVTGCHPDMAAPAGLNVNGDHYIVLATGGT				211
Qy	180 FSSGSASITVS				190
Db	212 FSSGYARITVA				222

```

RESULT 15
US-10-237-386-24
: Sequence 24, Application US/10237386
: Publication No. US20030180895A1
: GENERAL INFORMATION:
: APPLICANT: Danisco A/S
: APPLICANT: Sribesen, Ole
: TITLE OF INVENTION: Xylanase Variants Having Altered Sensitivity to Xylanase Inhibitors
: FILE REFERENCE: 674509-2046
: CURRENT APPLICATION NUMBER: US/10/237,386
: PRIOR FILING DATE: 2002-12-06
: PRIOR APPLICATION NUMBER: PCT/SE01/00426
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: GB 0005585.5
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: GB 0015751.1
: PRIOR FILING DATE: 2000-06-27
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: patentin version 3.0
: SEQ ID NO 24
: LENGTH: 225
: TYPE: PRT
: ORGANISM: T. lanuginosus
: US-10-237-386-24

```

Query Match	61.8%;	Score 651.5;	DB 14;	Length 225;
Best Local Similarity	60.7%;	Pred. No. 1.3e-56;		
Matches 116;	Conservative 29;	Mismatches 45;	Indels 1;	Gaps 1
Qy	1	QTQTPGTGHNHYFYSSVNNDHGCVMTLGGCGFSSVNMNSGDPVCGKGMQPGTKNKVY	60	
Dp	32	QTTPNSEGHHDDYYSSWSDDGAQATYTNLEGGYTEZSMWDGNTLVGKGKMNGLNARAI	91	
Qy	61	NFGSGVNPNGNSYLVYWGMSRNPILIEYIVENFETVPSFGATKLEBYVCDGSGVDIYAT	120	
Dp	92	HFGGCVYQPNGNISYLVYWGTRNPFLVEYIVENFETYPDSSGADTDLGTECDGSIYALGT	151	
Qy	121	QRNNAISIGTATFTFYQSVSVARNRNRSSGVNTAHPFAAMQHGLTL-GTMDQIVYAVEKY	179	
Dp	152	TRNNAISIDGCTFTFYQSVSVARNDKRTSGTIVTGTHFPAMARAGLNNCGHYIVATVEKY	211	
Qy	180	FSSGSASTVVS	190	
Dp	212	FSSGVARITVA	222	

Search completed: June 30, 2004, 19:59:13
Job time : 37.25 secs

Query Match	61.8%;	Score 651.5;	DB 14;	Length 225;
Best Local Similarity	60.7%;	Pred. No. 1.3e-56;		
Matches 116;	Conservative 29;	Mismatches 45;	Indels 1;	Gaps 1
Qy	1	QTQTPGTGYNHYFYSYNNDDHGQVMTLGGCGFYSVMNSGDPVFGKGMQPGTKAKYI	60	
Dp	32	QTTPNSEGHHDDGYYSWSDDGAQATYTNLEGGYTEZSMDDGNLTVGKGKMNGLNARAI	91	
Qy	61	NFGSGYNPENGNSYLYLVGMSRNPILIEXYIVENFETYPSTGATKTLAEYVCDGSGVDIYAT	120	
Dp	92	HFGGVGYFPGNGNSYLLAVGWTRNPLVEYXIYVENFETYPDSSGADTDLGTECDGSIYALGT	151	
Qy	121	QRNNAISIGTATFTFYQYSVVRNRHSSGVNTAHPFAAMQHGLTL-GTMDQIVYAVEKY	179	
Dp	152	TRNNAISIDGCTFTFYQYYSVYQDKRSTGVTLGTHPFAAMRAGLNNCGHYIVYATVEKY	211	
Qy	180	FSSGSASTVVS	190	
Dp	212	FSSGVARITVA	222	

A:Reference number: S39883; MUID:94088442; PMID:8264524
 A:Accession: S39883
 A:Molecule type: DNA
 A:Residues: 1-223 <SAB>
 A:Cross-references: EMBL:567387; NID:9455906; PID:AA829346.1; PID:9455907
 A:Experimental source: strain QM6
 A:Accession: S39884
 A:Molecule type: protein
 A:Residues: 34-43;49-57;121-151,178-191 <SAB>
 C:Genetics:
 A:Gene: xln2
 A:Introns: 91/2
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-33/Domain: propeptide #status predicted <PRO>
 F:34-223/Product: endo-1,4-beta-xylanase II #status experimental <MAT>
 F:45-223/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:71,94/Binding site: carbohydrate (asn) (covalent) #status predicted
 F:110,121/Binding site: substrate (tyr) #status predicted
 F:119,210/Active site: Glu #status predicted

Query Match 93.5%; Score 986; DB 2; Length 223;
 Best Local Similarity 95.3%; Pred. No. 7,3e-71;
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 60
 DB 34 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 93
 QY 61 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 DB 94 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 153
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNMAQHGLTLGTMDYQIVAVEGYF 180
 DB 154 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTAHFNMAQOGLTLGTMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 3
 A44595
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIB (proteinase-sensitive) - fungus (Trichoderma viride)
 N:Alternate names: xylanase IIB
 C:Species: Trichoderma viride
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 13-Mar-1998
 C:Accession: A44595
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44595
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:86,177/Active site: Glu #status predicted
 F:126-127/Cleavage site: Pro-Ser (unidentified proteinase) #status predicted
 F:129-130/Cleavage site: Glu-Gly (unidentified proteinase) #status predicted

Query Match 92.4%; Score 974; DB 1; Length 190;
 Best Local Similarity 93.2%; Pred. No. 5.4e-70;
 Matches 177; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 60
 DB 1 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 60
 QY 61 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 DB 61 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNMAQHGLTLGTMDYQIVAVEGYF 180
 DB 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTAHFNMAQOGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 4
 A44594
 endo-1,4-beta-xylanase (EC 3.2.1.8) IIA - fungus (Trichoderma viride)
 N:Alternate names: xylanase IIA
 C:Species: Trichoderma viride
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 07-Nov-1997
 C:Accession: A44594
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44594
 A:Molecule type: protein
 A:Residues: 1-190 <YAG>
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:12-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:77,88/Binding site: substrate (tyr) #status predicted
 F:86,177/Active site: Glu #status predicted

Query Match 91.4%; Score 963; DB 1; Length 190;
 Best Local Similarity 92.6%; Pred. No. 4e-69;
 Matches 176; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 1 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 60
 DB 1 OTTQPTGTHNGYFYSYWMDHGGVMTLGPGGQFVSNVNSGDFVGGKMGQPGTKNKVI 60
 QY 61 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 DB 61 NFSGYNPNNGSYLSVYGMGRNPLIEYIYVENFGTNPSTGATKLGAVTSDGSVYDIYRT 120
 QY 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTACHFNMAQHGLTLGTMDYQIVAVEGYF 180
 DB 121 QRVNAPSIEGTATFYQYWSVRNRHSSGSVNTAHFNMAQOGLTLGTMDYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 5
 A44593
 endo-1,4-beta-xylanase (EC 3.2.1.8) [validated] - fungus (Trichoderma harzianum) (strain N:Alternate names: xylanase
 C:Species: Trichoderma harzianum
 C>Date: 27-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Sep-2000
 C:Accession: A44593
 R:Yaguchi, M.
 submitted to the Protein Sequence Database, March 1994
 A:Reference number: A44593
 A:Accession: A44593
 A:Molecule type: protein

A;Residues: 1-190 <YAG>
 A;Experimental source: strain E58
 R;Campbell, R.L.; Rose, D.R.
 submitted to the Brookhaven Protein Data Bank, June 1994
 A;Reference number: A52868; PDB:1XND
 A;Contents: annotation; X-ray crystallography, 1.8 angstroms, residues 1-46; A'48-190
 C;Function:
 A;Description: catalyzes the hydrolysis of 1,4-beta-xyloridic bonds in xylians
 C;Pathway: xylan degradation
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
 F;1-190/Domain: endo-1,4-beta-xylanase homology <XYL>
 F;86,177/Active site: Glu #status experimental

Query Match 90.4%; Score 953; DB 1; Length 190;
 Best Local Similarity 91.6%; Pred. No. 2.5e-66;
 Matches 174; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 QTIOPGTGYNHGYFYSYNDGHHGVTWTLGPQGQFYSYNSGDFVGGKMGQGTAKKYI 60
 DB 1 QTIOPGTGYSNGYYSYNDGHHGVTYTNCGGGSFYVNSGNGFVGGKMGQGTAKKYI 60
 QY 61 NFSSSYNPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRT 120
 DB 61 NFSSSYNPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTSDDGVYDIYRT 120
 QY 121 QRVAPSIETATPFYQWYSVRNRHSSGSVNTACHFNMAHQHGLTGMDOYQIVAEVGF 180
 DB 121 QRVAPSIETATPFYQWYSVRNRHSSGSVNTANHFMAHQHGLTGMDOYQIVAEVGF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 6

endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Chaetomium gracile
 C;Species: Chaetomium gracile
 C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C;Accession: S71473; S78207
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asf
 A;Reference number: S71472; MUID:96118924; PMID:8595661
 A;Accession: S71473
 A;Molecule type: DNA
 A;Residues: 1-241 <YOS>
 A;Cross-references: EMBL:D49851; NID:q1339859; PIDD:BA08650.1; PID:q1339860
 A;Accession: S78207
 A;Molecule type: protein
 A;Residues: 38-44;89-91;153-161 <YOH>
 C;Genetics:
 A;Insertions: 88/2
 C;Function:
 A;Pathway: xylan degradation
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-241/Product: endo-1,4-beta-xylanase B #status predicted <MAT>
 F;43-220/Domain: endo-1,4-beta-xylanase homology <XYL>
 F;116,207/Active site: Glu #status predicted

Query Match 70.2%; Score 739.5; DB 2; Length 241;
 Best Local Similarity 71.6%; Pred. No. 2.3e-51;

Matches 131; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGHNGYFYSYNDGHHGVTWTLGPQGQFYSYNSGDFVGGKMGQGTAKKYINFSGSY 66
 DB 38 TGHNGYFYSYNDGHHGVTWTLGPQGQFYSYNSGDFVGGKMGQGTAKKYINFSGSY 66
 QY 67 NPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRTQVNA 126
 DB 67 NPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRTQVNA 126

DB 97 NPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRTQVNA 156
 QY 127 SIEGTATPFYQWYSVRNRHSSGSVNTACHFNMAHQHGLTGMDOYQIVAEVGFSSGSAS 186
 DB 157 SIEGTATPFYQWYSVRNRHSSGSVNTACHFNMAHQHGLTGMDOYQIVAEVGFSSGSAT 216
 QY 187 ITV 189
 DB 217 VNV 219

RESULT 7

endo-1,4-beta-xylanase (EC 3.2.1.8) A precursor - Chaetomium gracile
 S71472
 N;Alternate names: xylanase A
 C;Species: Chaetomium gracile
 C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 20-Jun-2000
 C;Accession: S71472; S78206
 R;Yoshino, S.; Oishi, M.; Moriyama, R.; Kato, M.; Tsukagoshi, N.
 Curr. Genet. 29, 73-80, 1995
 A;Title: Two family G xylanase genes from Chaetomium gracile and their expression in Asf
 A;Reference number: S71472; MUID:96118924; PMID:8595661
 A;Accession: S71472
 A;Molecule type: DNA
 A;Residues: 1-219 <YOS>
 A;Cross-references: EMBL:D49850; NID:q1339857; PIDD:BA08649.1; PID:q1339858
 A;Accession: S78206
 A;Molecule type: protein
 A;Residues: 31-45;82-94;152-160 <YOH>
 C;Genetics:
 A;Insertions: 81/2
 C;Function:
 A;Pathway: xylan degradation
 C;Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-219/Product: endo-1,4-beta-xylanase A #status experimental <MAT>
 F;42-219/Domain: endo-1,4-beta-xylanase homology <XYL>
 F;115,206/Active site: Glu #status predicted

Query Match 64.4%; Score 678.5; DB 2; Length 219;
 Best Local Similarity 65.9%; Pred. No. 1.4e-46;
 Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGHNGYFYSYNDGHHGVTWTLGPQGQFYSYNSGDFVGGKMGQGTAKKYINFSGS 65
 DB 36 GTGHNGYFYSYNDGHHGVTWTLGPQGQFYSYNSGDFVGGKMGQGTAKKYINFSGS 94
 QY 66 YNPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRTQVNA 125
 DB 96 YNPNNGSYISYVGSWRNPLIEYIYVENFGTYNPGTAKTGLGVTCDDGVYDIYRTQVNA 154
 QY 126 PSIEGTATPFYQWYSVRNRHSSGSVNTACHFNMAHQHGLTGMDOYQIVAEVGFSSGS 185
 DB 155 PSIEGTATPFYQWYSVRNRHSSGSVNTACHFNMAHQHGLTGMDOYQIVAEVGFSSGS 214
 QY 186 SITVS 190
 DB 215 SITVS 219

RESULT 8

JC7577
 endo-1,4-beta-xylanase (EC 3.2.1.8) G2 - Aspergillus oryzae
 N;Alternate names: endo-1,3-beta-xylanase G2; xylanase G2
 C;Species: Aspergillus oryzae
 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 03-Aug-2001
 C;Accession: JC7577; PC7120
 R;Kimura, T.; Suzuki, H.; Funahashi, H.; Aburatani, T.; Morimoto, K.; Karita, S.; Sakka
 Biosci. Biotechnol. Biochem. 64, 2794-2798, 2000
 A;Title: Molecular cloning, overexpression, and purification of a major xylanase from A.
 A;Reference number: JC7577; MUID: 21077500; PMID:11210150
 A;Accession: JC7577

A:Accession: EC7086
 A:Molecule type: protein
 A:Residues: 32-51 <K12>
 C:Genetics:
 A:Gene: xynA
 A:Introns: 89/2
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycoprotein; glycosidase; hydrolase

Query Match 58.8%; Score 620; DB 2; Length 221;
 Best Local Similarity 59.2%; Pred. No. 5,8e-42;
 Matches 113; Conservative 30; Mismatches 46; Indels 2; Gaps 2;

QY 1 QTIQPG-TGYNNGFYFYVNDHGCGVTMTLGPQGQFVSVMNSGDPVGGKMGQPTKTKV 59
 DB 32 QTISSQGTNNGGYYSFWTNGGCTVQYTNAGAEVSVTWENCDFTSKGWMTGSA-RD 90
 QY 60 INFSGSYNPNNGSYLAVYGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYR 119
 DB 91 ITFGGTNPSCNATLAYGWTTSPLVEYIIEIDYDYNPGSMYTKGTVTSDSVDIYE 150
 QY 120 TORVADPISGTAIFYVWSYVRNRHSSGSVNTACHFNMAHQGLTLGMDYQIVAVEGY 179
 DB 151 HQQVNOPSISGTAIFYVWSYVRNRHSSGSVNTACHFNMAHQGLTLGMDYQIVAVEGY 220
 QY 180 FSSGSASITVS 190
 DB 211 ESSGSSTITVS 221

RESULT 12

S43919
 endo-1,4-beta-xylanase (EC 3.2.1.8) precursor - imperfect fungus (Humicola insolens)
 C:Species: Humicola insolens
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
 A:Accession: S43919
 R:Dalboe, H.; Heidt-Hansen, H.P.
 Mol. Gen. Genet. 243, 253-260, 1994
 A:Title: A novel method for efficient expression cloning of fungal enzyme genes.
 A:Reference number: S43919; MUID:94247364; PMID:8190078
 A:Accession: S43919
 A:Molecule type: mRNA
 A:Residues: 1-227 <DAL>
 A:Cross-references: EMBL:X76047; NID:9505260; PIDN:CAA53632.1; PID:9505261
 C:Genetics:
 A:Gene: XY11
 C:Function:
 A:Pathway: xylan degradation
 C:Superfamily: endo-1,4-beta-xylanase; endo-1,4-beta-xylanase homology
 C:Keywords: glycosidase; hydrolase; polysaccharide degradation
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-227/Product: endo-1,4-beta-xylanase #status predicted <MAT>
 F:48-225/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:112,123,157/Binding site: substrate (Tyr, Tyr, Arg) #status predicted
 F:121,212/Active site: Glu #status predicted

Query Match 56.5%; Score 595.5; DB 2; Length 227;
 Best Local Similarity 57.1%; Pred. No. 5.1e-40;
 Matches 104; Conservative 26; Mismatches 51; Indels 1; Gaps 1;

QY 8 GYHNGFYFYVNDHGCGVTMTLGPQGQFVSVMNSGDPVGGKMGQPTKTKVINSGSYN 67
 DB 44 GWHNGFYFYVNDHGCGVTMTLGPQGQFVSVMNSGDPVGGKMGQPTKTKVINSGSYN 102
 QY 68 PNGNSYLYVGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYFORVNPAS 127
 DB 103 PQNGSLAYVGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYFORVNPAS 162
 QY 128 IESTATIFYVWSYVRNRHSSGSVNTACHFNMAHQGLTLGMDYQIVAVEGYFSSGSASI 187
 DB 163 IDSTRFQQWYSIRKNKRVGSVMNHNMAQOHGMPLGQHYQVAVATEGYQSSGESPI 222
 QY 188 TV 189

DB 223 YV 224

RESULT 13

JS0590
 endo-1,4-beta-xylanase (EC 3.2.1.8) B precursor - Streptomyces lividans
 N:Alternate names: xylanase B
 C:Species: Streptomyces lividans
 C:Date: 10-Mar-1994 #sequence_revision 22-Nov-1996 #text_change 26-Feb-1999
 A:Accession: JS0590; PS0239
 R:Shateck, F.; Roy, C.; Yaguchi, M.; Morosoli, R.; Kluepfel, D.
 Gene 107, 75-82, 1991
 A:Title: Sequences of three genes specifying xylanases in Streptomyces lividans.
 A:Reference number: JS0589; MUID:92077439; PMID:1743521
 A:Accession: JS0590
 A:Molecule type: DNA
 A:Residues: 1-333 <SHA>
 A:Cross-references: GB:M64552
 A:Accession: PS0239
 A:Molecule type: protein
 A:Residues: 41-71 <SH2>
 C:Genetics:
 A:Gene: xlnB
 C:Function:
 A:Description: catalyzes the hydrolysis of 1,4-beta-xylansidic bonds in xylans
 A:Pathway: xylan degradation
 C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
 C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
 F:1-40/Domain: signal sequence #status predicted <SIG>
 F:41-333/Product: endo-1,4-beta-xylanase B #status experimental <MAT>
 F:54-230/Domain: endo-1,4-beta-xylanase homology <XYL>
 F:127,217/Active site: Glu #status predicted

Query Match 55.2%; Score 582; DB 1; Length 333;
 Best Local Similarity 53.5%; Pred. No. 9.2e-39;
 Matches 106; Conservative 35; Mismatches 41; Indels 16; Gaps 5;

QY 5 PGT-----GYHNGFYFYVNDHGCGVTMTLGPQGQFVSVMNSGDPVGGKMGQ 52
 DB 35 PGTAAQADTVVTTNMGCTNNGGYYSFWTNGGCTVQYTNAGAEVSVTWENCDFTSKGWMTGSA-RD 94
 QY 53 PGTKKVNFSGSYNPNNGSYLAVYGMGRNPLIEYIVENFGTNPSTGATKLGAVTCDG 112
 DB 95 NGR-RITVQISGFSPSCNATLAYGWTTSPLVEYIIEIDYDYNPGSMYTKGTVTSDSVDIYE 151
 QY 113 SVYDIYFORVNPASISGTAIFYVWSYVRNRHSSGSVNTACHFNMAHQGLTLGMD-Y 171
 DB 152 GTYDIYKTRVNPKSVEGTRTFPDQWYSVRNRHSSGSVNTACHFNMAHQGLTLGMD-Y 211
 QY 172 QIVAVEGYFSSGSASITV 189
 DB 212 MIMATEGYQSSGTSISNV 229

RESULT 14

TS0601
 endo-1,4-beta-xylanase (EC 3.2.1.8) B, secreted [imported] - Streptomyces coelicolor
 N:Alternate names: xylanase B
 C:Species: Streptomyces coelicolor
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
 A:Accession: TS0601
 R:Redenbach, M.; Kleser, H.M.; Denaparte, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopa
 Mol. Microbiol. 21, 77-96, 1996
 A:Title: A set of ordered cosmid and a detailed genetic and physical map for the 8 Mb
 A:Reference number: Z20556; MUID:97000351; PMID:8843436
 A:Accession: TS0601
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-335 <RED>
 A:Cross-references: EMBL:AL333220; PIDN:CAB61738.1
 A:Experimental source: strain A3(2)
 C:Genetics:

A:Gene: xlnB
C:Superfamily: Clostridium endo-1,4-beta-xylanase B; endo-1,4-beta-xylanase homology
C:Keywords: glycosidase, hydrolase

Query Match

55.2%; Score 582; DB 2; Length 335;

Best Local Similarity 54.0%; Pred. No. 9.3e-39; Mismatches 42; Indels 16; Gaps 5;

Matches 107;

Conservative 33;

Mismatches 42;

Indels 16;

Gaps 5;

5 PGT-----GHNQYFYSYWNDDHGVTMTLGPQGQFSVWMSNSGDFVQKGMQ 52

DB 36 PGTAGQADTVTTTQEGTNGYYSFTDQGTVMNSGQYSTSWRTGNFVAGKGM 95

QY 53 PGTAKVINFSGSYNPNNGSYLSVYGSNPLIEYIVENPGTYNPSTGATKLGVTCDG 112

DB 96 NGGR-RTVQYSGSFNPSGNAYLALYGMTSNPLVEYIVDNGTYRP-TGEYK-GTVSDG 152

QY 113 SVYDPIRTQYVNPSTEGTATFEYQVWSVRNRHSSGVSNTACHFNMAQGLTLGTM-D-Y 171

DB 153 GTYDITKTRVKNPSEVGRITFDQVWSVRQAKRTGTTTGNHFDMAAGMPLGNFSY 212

QY 172 QIVAVEGYFSSGSASITV 189

DB 213 MIVATEGYSSGSSSINV 230

RESULT 15

140712 endo-1,4-beta-xylanase (EC 3.2.1.8) D precursor - Cellulomonas fimi

N:Alternate names: xylanase D

C:Species: Cellulomonas fimi

C>Date: 16-Aug-1996 #sequence_revision 22-Nov-1996 #text_change 18-Jun-1999

C:Accession: 140712 R:Millward-Sadler, S.J.; Poole, D.M.; Henriessat, B.; Hazlewood, G.P.; Clarke, J.H.; Gilh

Mol. Microbiol. 11, 375-382, 1994

A:Title: Evidence for a general role for high-affinity non-catalytic cellulose binding

A:Reference number: 140712; PMID:94224155; PMID:8170389

A:Accession: 140712

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-644 <RES>

A:Cross-references: EMBL:X76729; NID:9558176; PID:CAA54145.1; PID:9558177

C:Genetics:

A:Gene: xynD

C:Function:

A:Description: catalyzes the hydrolysis of 1,4-beta-xylosidic bonds in xylans

C:Superfamily: Cellulomonas endo-1,4-beta-xylanase D; endo-1,4-beta-xylanase homology; r

C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:1-35/Domain: signal sequence #status predicted <SIG>

F:36-644/Product: endo-1,4-beta-xylanase D #status predicted <WAT>

F:54-229/Domain: endo-1,4-beta-xylanase homology <XVL>

F:361-508/Domain: noB homology <NOB>

F:126,216/Active site: Glu #status predicted

Query Match 55.1%; Score 580.5; DB 1; Length 644;

Best Local Similarity 56.2%; Pred. No. 2.5e-38;

Matches 104; Conservative 37; Mismatches 39; Indels 5; Gaps 4;

QY 7 TCHNNGYFYSYWNDDHGVTMTLGPQGQFSVWMSNSGDFVQKGMQPGTKXKYNIFSGSY 66

DB 49 TGHGQYFYSFWTDSFGSVSMDLNSGGYT-RMSNTGNFVAGKGMSTGR-KTVSYSGCF 106

QY 67 NPNNGSYLSVYGSNPLIEYIVENPGTYNPSTGATKLGVTCDGVSVDIYRTQVNA 126

DB 107 NPSRAVYLTIGWTSPLVEYIVDSWQTYRPT--GTFMGVTSDDGTYDIYRTQVNA 164

QY 127 STEG-TATFYQWVSRRNRHSSGVSNTACHFNMAQGLTLGTMDOIVAVEGYFSSGSA 185

DB 165 SIEGDSSTFYQWVSRRNRHSSGVSNTACHFNMAQGLTLGTMDOIVAVEGYFSSGSA 224

QY 186 SITVS 190

DB 225 SITVS 229

Search completed: June 30, 2004, 19:41:14
Job time : 13 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:34:09 ; Search time 7.25 seconds
(without alignments)
1364.597 Million cell updates/sec

Title: US-09-856-025B-65
Perfect score: 1054
Sequence: 1 QTIQPTGTNGYFYSYMND.....YQIVAVEGYRSGSASITVS 190

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	986	93.5	222	1 XYN2_TRIRE	P36217 trichoderma
2	947	89.8	190	1 XYN2_TRIRE	P48793 trichoderma
3	658.5	62.5	225	1 XYN1_EMENTI	P55332 emeticella
4	651.5	61.8	225	1 XYN2_THEMA	O43057 thermomyces
5	644.5	61.1	221	1 XYN2_EMENTI	P55333 emeticella
6	644.5	61.1	225	1 XYN2_ASPPA	P48824 aspergillus
7	632.5	60.0	225	1 XYN2_ASPPA	P55330 aspergillus
8	626.5	59.4	221	1 XYN1_COCOA	O06562 cochlidiobol
9	595.5	56.5	227	1 XYN1_HUMIN	P55334 humicola in
10	585	55.5	335	1 XYN2_STRLI	P26515 streptomyces
11	580.5	55.1	644	1 XYN2_CELFI	P54865 cellulomonas
12	572.5	54.3	197	1 XYN1_SCHCO	P35809 schizophyll
13	552.5	52.4	233	1 XYN2_MAGGR	P55335 magnaporthe
14	533	50.6	240	1 XYN2_STRLI	P26220 streptomyces
15	506.5	48.1	210	1 XYN2_BACST	P45705 bacillus st
16	494	46.9	213	1 XYN2_BACST	P18429 bacillus su
17	493	46.8	213	1 XYN2_BACCT	P09860 bacillus cl
18	463	43.9	228	1 XYN2_BACPU	P00694 bacillus pu
19	451.5	42.8	261	1 XYN2_CLOSA	PI17137 clostridium
20	450	42.7	512	1 XYN2_CLOSR	P33558 clostridium
21	430.5	40.8	229	1 XYN1_TRIRE	P36218 trichoderma
22	417	39.6	211	1 XYN3_ASPPA	P33557 aspergillus
23	416	39.5	211	1 XYN1_ASPPA	P55329 aspergillus
24	416	39.5	211	1 XYN1_ASPPG	P55329 aspergillus
25	414	39.3	211	1 XYN1_ASPTU	P55331 aspergillus
26	391	37.1	954	1 XYN2_RUMFL	P29126 rumiobacillus
27	386.5	36.7	179	1 XYN2_PSEXY	P33533 pseudobutyri
28	379.5	36.0	802	1 XYN2_RUMFL	O33317 rumiobacillus
29	302	28.7	607	1 XYN2_NEOPA	P59127 neocallimast
30	298.5	28.3	608	1 XYN2_FIRSP	P55811 fibrobacter
31	259	24.6	625	1 XYN2_FIRSP	Q12667 fibrobacter
32	93	8.8	414	1 PHA1_PSEDE	P52050 pseudomonas
33	92.5	8.8	1592	1 SORL_CHICK	Q98930 g sortilin

ALIGNMENTS

RESULT 1	ID	XYN2_TRIRE	STANDARD;	PRT;	222 AA.
AC	P36217;				
DT	01-UTN-1994 (rel. 29, Created)				
DT	01-UTN-1994 (rel. 29, Last sequence update)				
DT	28-FEB-2003 (rel. 41, Last annotation update)				
DE	Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)				
DE	(1,4-beta-D-xylan xylanohydrolase 2).				
GN	XYN2.				
OS	Trichoderma reesei (Hypocrea jecorina).				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
OC	Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.				
OX	NCBI_Taxid=51453;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN=C30;				
RX	MEDLINE=93103679; PubMed=1369024;				
RA	Toerrien A., Mach R.L., Messner R., Gonzalez R., Kalkkinen N.,				
RA	Harkki A., Kubicek C.P.;				
RT	"The two major xylanases from Trichoderma reesei: characterization of				
RT	both enzymes and genes."				
RL	Biotechnology 10:1461-1465(1992).				
RN	[2]				
RP	X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=94283373; PubMed=8013449;				
RA	Toerrien A., Harkki A., Rouvinen J.;				
RT	"Three-dimensional structure of endo-1,4-beta-xylanase II from				
RT	Trichoderma reesei: two conformational states in the active site."				
RL	EMBO J. 13:2493-2501(1994).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=95127663; PubMed=7827044;				
RA	Toerrien A., Rouvinen J.;				
RT	"Structural comparison of two major endo-1,4-xylanases from				
RT	Trichoderma reesei."				
RL	Biochemistry 34:847-856(1995).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).				
RC	STRAIN=C30;				
RX	MEDLINE=96302263; PubMed=8755744;				
RA	Havulinainen R., Toerrien A., Laitinen T., Rouvinen J.;				
RT	"Covalent binding of three epoxypyl xylosides to the active site of				
RT	endo-1,4-xylanase II from Trichoderma reesei."				
RL	Biochemistry 35:9617-9624(1996).				
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic				
CC	linkages in xylans.				
CC	-1- PATHWAY: Xylan degradation.				
CC	-1- PTM: The N-terminus is blocked.				
CC	-1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl				
CC	hydrolases).				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				

34	91.5	8.7	479	1	BGLA_ECOLI	O46829 escherichia
35	91.5	8.7	795	1	D152_HAEIN	P44935 haemophilus
36	91	8.6	483	1	PASC_XENLA	O91837 xenopus lae
37	90.5	8.6	797	1	D151_HAEIN	O46024 haemophilus
38	90	8.5	793	1	D153_HAEIN	O32629 haemophilus
39	90	8.5	1829	1	FRPC_NEIMB	O93455 neisseria m
40	89.5	8.5	366	1	OM3A_EHIV	O05811 rhizobium l
41	89.5	8.5	666	1	MUR2_ENTHR	P39046 enterococcus
42	88.5	8.4	352	1	A85C_MYCAV	O52972 mycobacteri
43	88	8.3	1115	1	FRPA_NEIMC	P55126 neisseria m
44	88	8.3	1829	1	FRPC_NEIMC	P55127 neisseria m
45	87.5	8.3	729	1	FHUE_ECOLI	P16869 escherichia

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 CC or send an email to license@1sb-sib.ch).

DR EMBL: X69573; CAA9293.1; -
 DR PIR: S39154; S39154
 DR PDB: 1X9C; 08-AUG-95.
 DR PDB: 1XYP; 08-AUG-95.
 DR PDB: 1ENX; 08-AUG-95.
 DR PDB: 1RED; 11-JAN-97.
 DR PDB: 1REF; 11-JAN-97.
 DR PDB: 1REF; 11-JAN-97.
 DR InterPro: IPR008985; ConA_like lec_g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11.
 DR PRINTS: PR00911; GLYCOSYL_HYDROL_F11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
 KW 3D-structure.
 FT SIGNAL 1 32
 FT CHAIN 1 32
 FT ACT_SITE 118 118 ENDO-1,4-BETA-XYLANASE 2.
 FT ACT_SITE 209 209 NUCLEOPHILE.
 FT CARBOHYD 70 70 PROTON DONOR.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT STRAND 34 35
 FT TURN 38 42
 FT TURN 43 44
 FT STRAND 45 51
 FT TURN 57 61
 FT STRAND 64 65
 FT TURN 66 71
 FT STRAND 76 83
 FT STRAND 91 101
 FT STRAND 104 113
 FT TURN 114 116
 FT STRAND 117 125
 FT TURN 130 133
 FT STRAND 135 142
 FT TURN 143 144
 FT STRAND 145 157
 FT TURN 160 161
 FT STRAND 164 173
 FT STRAND 180 183
 FT HELIX 184 193
 FT TURN 194 195
 FT STRAND 200 211
 FT STRAND 214 222
 SQ SEQUENCE 222 AA; 24172 MW; 15F7032FACF963FF CRC64;
 Query Match 93.5%; Score 986; DB 1; Length 222;
 Best Local Similarity 95.3%; Pred. No. 2,7e-76;
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

RESULT 2
 ID XYN_TRIHA STANDARD; PRT; 190 AA.
 AC P48793;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8) (Xylanase) (1,4-beta-D-xylan
 DE xylanohydrolase).
 OS Trichoderma harzianum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
 OX NCBI_Taxid=5544;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=E58;
 RA Yaeguchi M., Roy C., Watson D.C., Rollin F., Tan L.U.L., Senior D.J.,
 RA Sadtler U.N.;
 RT "The amino acid sequence of the 20 kD xylanase from Trichoderma
 RT harzianum E58.";
 RL (In) Visser J., Beldman G., Kuipers-van Sommeren M.A.,
 RL Voregen A.G.J. (eds.);
 RL Xylans and xylanases, pp.435-438, Elsevier, Amsterdam (1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Campbell R.L., Rose D.R., Wakarchuk W.W., To R.J., Sung W.,
 RA Yaeguchi M.;
 RT "High-resolution structures of xylanases from B.circulans and
 RT T.harzianum identify a new folding pattern and implications for the
 RT atomic basis of the catalysis.";
 RL (In) Suominen P., Reinikainen T. (eds.);
 RL Trichoderma reesei cellulases and other hydrolases, pp.63-72,
 RL Foundation for Biotechnical and Industrial Fermentation Research,
 RL Helsinki (1993).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylansidic
 CC linkages in xylans.
 CC -!- PATHWAY: Xylan degradation.
 CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC PDB: 1XND; 20-DEC-94.
 DR InterPro: IPR008985; ConA_like lec_g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; 3D-structure.
 FT ACT_SITE 86 86 NUCLEOPHILE.
 FT ACT_SITE 177 177 PROTON DONOR.
 FT STRAND 3 3
 FT STRAND 6 9
 FT STRAND 14 19
 FT STRAND 25 29
 FT TURN 32 33
 FT STRAND 34 39
 FT STRAND 44 51
 FT TURN 56 57
 FT STRAND 59 69
 FT TURN 72 81
 FT STRAND 82 84
 FT STRAND 85 93
 FT STRAND 98 101
 FT STRAND 103 110
 FT TURN 111 112
 FT STRAND 113 125
 FT TURN 128 129
 FT STRAND 132 141
 FT STRAND 148 151
 FT HELIX 152 161
 FT TURN 162 163
 FT STRAND 168 179

FT STRAND 182 190
SQ SEQUENCE 190 AA; 20703 MW; 6A0F4D1C3599C698 CRC64;
Query Match 89.8%; Score 947; DB 1; Length 190;
Best Local Similarity 91.1%; Pred. No. 4,3e-73;
Matches 13; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 1 QTTQPGTGHNGYFFSYWMDHGCVMTLGPQGQFVYVNSNSGDPVGGKMGQGTNKKVY 60
DB 1 QTTGPGTGYSGYYSYWMDGHAGVTYTNKGSGSFYVNSNSGDFVAGKMGQPGTNNKYI 60
QY 61 NFGSGYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGEXTCDGSVVDIYRT 120
DB 61 NFGSGYNPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGEXTCDGSVVDIYRT 120
QY 121 QRVNAPSIEGTATFYQVWSVRNRHSSGSVNTACHFNMAOHGLTLGTMDYQIVAVEGYF 180
DB 121 QRVNAPSIIETATFYQVWSVRNRHSSGSVNTANHNFNMAASHGLTLGTMDYQIVAVEGYF 180
QY 181 SSGSASITVS 190
DB 181 SSGSASITVS 190

RESULT 3
XYNA_EMBL
ID XYNA_EMBL STANDARD; PRT; 225 AA.
AC P55352; 000173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosidase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE (1,4-beta-D-xylosyl xylanohydrolase 1).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236210; PubMed=8787417;
RA Perez-Gonzalez J.A., de Graaf L.H., Visser J., Ramon D.;
RT "Molecular cloning and expression in *Saccharomyces cerevisiae* of two
RT *Aspergillus nidulans* xylanase genes.";
RL Appl. Environ. Microbiol. 62:2179-2182(1996).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z49892; CAA90073.1; -
CC PIR; S57477; S57477.
CC HSSP; P48793; 1XND.
CC InterPro; IPR008985; ConA_like_1ec_g1.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.
CC DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
CC DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KM Xylan degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1
FT CHAIN 1 225
FT ACT SITE 121 225 ENDO-1,4-BETA-XYLANASE 1.
FT ACT SITE 212 212 NUCLEOPHILE (BY SIMILARITY).
FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 225 AA; 24070 MW; 670F2C79602C7FEC CRC64;

Query Match 62.5%; Score 658.5; DB 1; Length 225;
Best Local Similarity 64.5%; Pred. No. 1.1e-48;
Matches 118; Conservative 25; Mismatches 39; Indels 1; Gaps 1;

QY 7 TGHNGYFYSWMDHGCVMTLGPQGQFVYVNSNSGDPVGGKMGQGTNKKVY 66
DB 43 TGSNGYYSFMTDGGGVITNAGGSYVQMSVNGVFGKMGKMPQS-TRTINYGGSF 101
QY 67 NPNNGSYLSYVGMGRNPLIEYIYVENFGTNPSTGATKLGEXTCDGSVVDIYRTQVNAAP 126
DB 102 NPSGNGYLAAYGWTQNPPLIEYIYVESYCTNPGSGGGRGTVSDGATYDITATRVNAP 161
QY 127 SIEGATFYQVWSVRNRHSSGSVNTACHFNMAOHGLTLGTMDYQIVAVEGYFSSGSAS 186
DB 162 SIEGATFEQFWSVRQSKRTGTVTANHFNMAALGLRGTNHYQIVAVEGYSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 4
XYNA_THELA
ID XYNA_THELA STANDARD; PRT; 225 AA.
AC O43057;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylosidase 1 precursor (EC 3.2.1.8) (Xylanase 1)
DE Xylan xylanohydrolase).
GN XYNA.
OS Thermomyces lanuginosus (Humicola lanuginosa).
OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Thermomyces.
OC NCBI_TaxID=53411;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=97033440; PubMed=8879171;
RA Schlacher A., Holzmann K., Hayn M., Steiner W., Schwab H.;
RT "Cloning and characterization of the gene for the thermostable
RT xylanase Xyna from *Thermomyces lanuginosus*.";
RL J. Biotechnol. 49:211-218(1996).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.55 ANGSTROMS).
RC STRAIN=DSM 5826 / Tsiklinsky;
RX MEDLINE=98426042; PubMed=9753433;
RA Gruber K., Klinechar G., Hayn M., Schlacher A., Steiner W.,
RA Kracky C.;
RT "Thermophilic xylanase from *Thermomyces lanuginosus*: high-resolution
RT X-ray structure and modeling studies.";
RL Biochemistry 37:13475-13485(1998).
CC -1- FUNCTION: THERMOSTABLE XYLANASE.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC
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CC
CC EMBL; U35436; AAB94633.1; -
CC PDB; 1YNA; 12-FEB-97.
CC InterPro; IPR008985; ConA_like_1ec_g1.
CC InterPro; IPR001137; Glyco_hydro_11.
CC Pfam; PF00457; Glyco_hydro_11; 1.
CC PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE: PS00776; GLYCOSYL HYDROL F11.1; 1.
 DR PROSITE: PS00777; GLYCOSYL HYDROL F11.2; 1.
 KM xylan degradation; Hydrolyase; Glycosidase; Signal; 3D-structure;
 KM Pyridone carboxylic acid.
 FT SIGNAL 1 31
 FT CHAIN 32 225
 FT ACT SITE 117 117 ENDO-1,4-BETA-XYLANASE.
 FT ACT SITE 209 209 NUCLEOPHILE.
 FT MOD RES 32 32 PROTON DONOR.
 FT DISULFID 141 185 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 33 33
 FT STRAND 37 37
 FT TURN 37 41
 FT TURN 42 43
 FT STRAND 44 50
 FT STRAND 56 60
 FT TURN 63 64
 FT STRAND 65 70
 FT STRAND 75 82
 FT STRAND 90 100
 FT STRAND 103 112
 FT TURN 113 115
 FT STRAND 116 124
 FT TURN 129 132
 FT STRAND 134 141
 FT TURN 142 143
 FT STRAND 144 158
 FT TURN 159 160
 FT STRAND 161 172
 FT STRAND 179 182
 FT HELIX 183 192
 FT TURN 193 194
 FT STRAND 200 211
 FT STRAND 214 223
 SQ SEQUENCE 225 AA; 24355 MM; FAA79A914C5C676C CRC64;
 Query Match 61.8%; Score 651.5; DB 1; Length 225;
 Best Local Similarity 60.7%; Pred. No. 4.3e-48;
 Matches 116; Conservative 29; Mismatches 45; Indels 1; Gaps 1;
 QY 1 QTTQPTGYNGYFYIYNDGSGVTMTLPGGQGFVNMNSGDPYFGKGMQPGTKNKYI 60
 DB 32 QTPNSEGWDGYYYSWMSDGAQATYTNLEGGTYEISWGDGNTLVGKGMNPGANARAI 91
 QY 61 NFGSNPNNGNSYLSYSGMRNPLIEYIYENFGTNPSTGATKLGAVTCDSVYDIYRT 120
 DB 92 HFGGVQPNNSYLAAYGMTRNPLVYIYENFGTIDPSSGATDLCIVACDSIYRLKXT 151
 QY 121 QRVNAPSIEGTAFYQYWSYVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 179
 DB 152 TRVNAPSIDGTQTFDDYWSYVRQDKRTSGTGTGCHFDAMARAGLANVNGDHYVQIVATGEGY 211
 QY 180 FSSGGSATYVS 190
 DB 212 FSSGYARITVA 222

RESULT 5
 XYN2_EMENTI STANDARD; PRT; 221 AA.

ID XYN2_EMENTI STANDARD; PRT; 221 AA.
 AC P55335; 000176;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 2 precursor (EC 3.2.1.8) (Xylanase 2)
 DE (1,4-beta-D-xylan xylanohydrolase 2).
 OS Aspergillus nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emmentella.
 OC NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96236210; Pubmed=8787417;
 RA Perez-Gonzalez J.A., de Graaff L.H., Visser J., Ramon D.;

RT "Molecular cloning and expression in Saccharomyces cerevisiae of two
 RT Aspergillus nidulans xylanase genes.";
 RT Appl. Environ. Microbiol. 62:2179-2182(1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 DR EMBL; Z49893; CA90074.1; -
 DR PIR; S57469; S57469.
 DR HSSP; P48793; 1XND.
 DR InterPro; IPR008985; Gna_1like_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDLASE11.
 DR PROSITE; PS00776; GLYCOSYL HYDROL F11.1; 1.
 DR PROSITE; PS00777; GLYCOSYL HYDROL F11.2; 1.
 KM xylan degradation; Hydrolyase; Glycosidase; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 221 ENDO-1,4-BETA-XYLANASE 2.
 FT ACT SITE 117 117 NUCLEOPHILE (BY SIMILARITY).
 FT ACT SITE 208 208 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 221 AA; 23517 MM; 4266R5E80DBE9475 CRC64;

Query Match 61.1%; Score 644.5; DB 1; Length 221;
 Best Local Similarity 64.1%; Pred. No. 1.6e-47;
 Matches 118; Conservative 26; Mismatches 39; Indels 1; Gaps 1;

QY 7 TGYNNGYFYIYNDGSGVTMTLPGGQGFVNMNSGDPYFGKGMQPGTKNKYINFGSY 66
 DB 39 TGTSGGYIYSPFMDGSDVYTNNDGGSYIVENTKCNFVFGKGMNNGS-SQITISYSGSP 97
 QY 67 NFGSNPNNGNSYLSYSGMRNPLIEYIYENFGTNPSTGATKLGAVTCDSVYDIYRT 126
 DB 98 IPGNGYLSYSGMRNPLIEYIYENFGTNPSTGATKLGAVTCDSVYDIYATRENAP 157
 QY 127 SIEGTAFYQYWSYVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 186
 DB 158 SIEGTAFYQYWSYVRNHRSSGSYNTACHFNMAQHGTLT-GTMDYQIVAVBGY 217
 QY 187 ITVS 190
 DB 218 ITVS 221

RESULT 6
 XYNB_ASPKA STANDARD; PRT; 225 AA.

ID XYNB_ASPKA STANDARD; PRT; 225 AA.
 AC P48824;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
 DE (1,4-beta-D-xylan xylanohydrolase B).
 GN XYNB.
 OS Aspergillus kawachi (Aspergillus awamori var. kawachi).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillaceae.
 OC NCBI_TaxID=40384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO 4308;
 RA Ito K.;
 RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.


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CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
CC hydrolases).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D38070; BAA07264.1; -.
CC HSSP: P36217; 1XCO.
CC InterPro: IPR008985; Cons 1 like lec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_2; 1.
CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KM Xylan degradation; Hydrolyase; Glycosidase; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 225
CC FT ACT SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 225 AA; 24146 MW; 54B13D48AF5C7115 CRC64;

Query Match 61.1%; Score 644.5; DB 1; Length 225;
Best Local Similarity 63.4%; Pred. No. 1.7e-47;
Matches 116; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

QY 7 TGYHNGFYFSYMNQDHGVTMTLPGGQFYSYMNWNSGDFVGGKMGQPGTKNKNVINFSGSY 66
DB 43 TGENNNGFYFSFWTDGGGVDVYTNAGNSYSVENWNGVFGKMGWPSA-KDITSGNF 101
QY 67 NPNGNSYLSYVGMSRNPLIEYIVENFGTYNPSGATKLGVTDCGSYDIYRQVNP 126
DB 102 TPGSGNGYLSYVGWTTDPLIEYIVESYGDYNPSSGSTRGNVSDGSYDIYARFTNP 161
QY 127 SIEGTAFTYQWYVRNRHSSGVSNTACHFNMAQHGILGMDVQIVAVEGYFSSGSAS 186
DB 162 SIQGTATFYQWYVRNRHSSGVSNTACHFNMAQHGILGMDVQIVAVEGYFSSGSAS 221
QY 187 ITV 189
DB 222 ITI 224

RESULT 7
XYN2 ASPNG STANDARD; PRT; 225 AA.
AC P55310; Q12557;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase II precursor (EC 3.2.1.8) (Xylanase II)
DE (1,4-beta-D-xylan xylanohydrolase II).
GN XYNB.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IFO 4066;
RA Ito K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
CC linkages in xylans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl

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CC hydrolases).
CC -----
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CC -----
CC EMBL: D38071; BAA07265.1; -.
CC HSSP: P09850; 1XNB.
CC InterPro: IPR008985; Cons 1 like lec_g1.
CC InterPro: IPR001137; Glyco_hydro_11.
CC Pfam: PF00457; Glyco_hydro_11; 1.
CC PRINTS: PR00911; GLHYDRASE11.
CC PROSITE: PS00776; GLYCOSYL_HYDROL_F11_2; 1.
CC DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
CC KM Xylan degradation; Hydrolyase; Glycosidase; Signal.
CC FT SIGNAL 1 18
CC FT CHAIN 19 37
CC FT ACT SITE 121 121 NUCLEOPHILE (BY SIMILARITY).
CC FT ACT SITE 212 212 PROTON DONOR (BY SIMILARITY).
CC SQ SEQUENCE 225 AA; 24057 MW; C4B8B007AB2B8FD CRC64;

Query Match 60.0%; Score 632.5; DB 1; Length 225;
Best Local Similarity 62.8%; Pred. No. 1.7e-46;
Matches 115; Conservative 25; Mismatches 42; Indels 1; Gaps 1;

QY 7 TGYHNGFYFSYMNQDHGVTMTLPGGQFYSYMNWNSGDFVGGKMGQPGTKNKNVINFSGSY 66
DB 43 TGENNNGFYFSFWTDGGGVDVYTNAGNSYSVENWNGVFGKMGWPSA-KDITSGNF 101
QY 67 NPNGNSYLSYVGMSRNPLIEYIVENFGTYNPSGATKLGVTDCGSYDIYRQVNP 126
DB 102 TPGSGNGYLSYVGWTTDPLIEYIVESYGDYNPSSGSTRGNVSDGSYDIYARFTNP 161
QY 127 SIEGTAFTYQWYVRNRHSSGVSNTACHFNMAQHGILGMDVQIVAVEGYFSSGSAS 186
DB 162 SIQGTATFYQWYVRNRHSSGVSNTACHFNMAQHGILGMDVQIVAVEGYFSSGSAS 221
QY 187 ITV 189
DB 222 ITV 224

RESULT 8
XYN1 COCCA STANDARD; PRT; 221 AA.
AC Q06562;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase I precursor (EC 3.2.1.8) (Xylanase I)
DE (1,4-beta-D-xylan xylanohydrolase I).
GN XYL1.
OS Cochliobolus carbonum (Bipolaris zeicola).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5017;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Race 1 / Isolate SB11;
RC MEDLINE=94003417; PubMed=8400376;
RA Apel P.C., Panaciotone D.G., Holden F.R., Walton J.D.;
RL "Cloning and targeted gene disruption of XYL1, a beta 1,4-xylanase
RL gene from the maize pathogen Cochliobolus carbonum.",
RN Mol. Plant Microbe Interact. 6:467-473(1993).
RP PARTIAL SEQUENCE.
RA Holden F.R., Walton J.D.;
RL "Xylanases from the fungal maize pathogen Cochliobolus carbonum.",

```

RL Physiol. Mol. Plant Pathol. 40:39-47(1992).
 CC - FUNCTION: MAJOR XYLAN-DEGRADING ENZYME. CONTRIBUTES TO THE
 CC HYDROLYSIS OF ARABINOXYLAN, THE MAJOR COMPONENT OF MAIZE CELL-
 CC WALLS.
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC - PATHWAY: Xylan degradation.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - FTM: The N-terminus is blocked.
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC -----
 CC EMBL: L13596; AAA33024.1; -.
 CC HSSP: O43097; 1YNA.
 DR InterPro: IPR008985; ConA like lec.gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; signal.
 FT SIGNAL 1 30
 FT CHAIN 1 30
 FT ACT_SITE 115 115
 FT ACT_SITE 206 206
 FT CONFLICT 81 81
 FT CONFLICT 107 107
 FT CONFLICT 131 131
 SQ SEQUENCE 221 AA; 23728 MW; 59DBD983FC5B8C CRC64;
 Query Match 59.4%; Score 626.5; DB 1; Length 221;
 Best Local Similarity 60.0%; Pred. No. 5.4e-46;
 Matches 114; Conservative 26; Mismatches 49; Indels 1; Gaps 1;
 QY 1 QITQPTGYHNGYFYVYNDHGCVMTLTGPGGQSFVSNMNSGDFVGGKMGQGTNKKYI 60
 DB 31 QNTPEEGTHNGCFWMSWDGAPATYTTGAGGSISVMSGSGNLVGGKMNPGTA-RTI 89
 QY 61 NFGSYNPNQNSYLSVYVGSRNPLIEYIYVENFGYVNPSTGATKLGVTCDGSVYDIYRT 120
 DB 90 TVSGTNYNNGSYLAVYVWTRNPLVEYVVENFGTYDPSSQSNKGTIVISDGSYKIAQS 149
 QY 121 QRVNAISIEGTAIFYQVYSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYF 180
 DB 150 TRTNQPSIDGTRTFQGYWVSVRQKRSVNMKTHFDAMASKMNLGQHYQIVATGEGIF 209
 QY 181 SSGSASITVA 190
 DB 210 STGNAQITVA 219
 RESULT 9
 XYN1 HUMIN STANDARD; PRT; 227 AA.
 ID XYN1 HUMIN
 AC P55334; O12625;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 1 precursor (EC 3.2.1.8) (Xylanase 1)
 DE (1,4-beta-D-xylan xylanohydrolase 1).
 GN XYL1.
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 OX NCBI_TaxID=34413;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=94247364; PubMed=8190078;
 RA Dabosge H.; Hansen H.P.H.;
 RT "A novel method for efficient expression cloning of fungal enzyme
 RT genes.";
 RL Mol. Gen. Genet. 243:253-260(1994).
 CC - CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC - PATHWAY: Xylan degradation.
 CC - SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X76047; CA53632.1; -.
 CC PIR: S43919; S43919.
 DR HSSP: O43097; 1YNA.
 DR InterPro: IPR008985; ConA like lec.gl.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRLASE1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Xylan degradation; Hydrolase; Glycosidase; signal.
 FT SIGNAL 1 19
 FT CHAIN 1 227
 FT ACT_SITE 121 121
 FT ACT_SITE 212 212
 FT ACT_SITE 212 212
 SQ SEQUENCE 227 AA; 25601 MW; 5C2FF6ADCFADAF CRC64;
 Query Match 56.5%; Score 595.5; DB 1; Length 227;
 Best Local Similarity 57.1%; Pred. No. 2.3e-43;
 Matches 104; Conservative 26; Mismatches 51; Indels 1; Gaps 1;
 QY 8 GYHNGYYSYVNDHGCVMTLTGPGGQSFVSNMNSGDFVGGKMGQGTNKKYINFGGSYV 67
 DB 44 GMHNGYYSYVNDHGCVMTLTGPGGQSFVSNMNSGDFVGGKMGQGTNKKYINFGGSYV 102
 QY 68 PNGSYYSYVGSNPNPLIEYIYVENFGYVNPSTGATKLGVTCDGSVYDIYRTQVNPAS 127
 DB 103 PQNGYLAIVGWTNPLVEYVIESYTYNPGSAQYKGFYDDGQYDIFVSTRYNQPS 162
 QY 128 IEGTATFYQVYSVRNRHSSGSVNTACHFNAMAQHGTLTGMDYQIVAVEGYFSSGAS 187
 DB 163 IDGTRTFQYWSIRKRVGGSVNMQNHFNAMOOHGMPLGQHYQIVATGEGYSSGSDI 222
 QY 188 TV 189
 DB 223 YV 224
 RESULT 10
 XYNB STRLI STANDARD; PRT; 335 AA.
 ID XYNB STRLI
 AC P26515;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase B precursor (EC 3.2.1.8) (Xylanase B)
 DE (1,4-beta-D-xylan xylanohydrolase B).
 GN XYNB.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-72.

```

RC STRAIN=66 / 1326;
RA MEDLINE=92077439; PubMed=1743521;
RX Sharack F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
RT "Sequences of three genes specifying xylanases in Streptomyces
   lividans.";
RN Gene 107:75-82(1991).
RP REVISIONS TO 29-32 AND 252-307.
RC STRAIN=66 / 1326;
RX MEDLINE=95189090; PubMed=7533741;
RA Sharack F., Biele P., Morosoli R., Kluepfel D.;
RT "Analysis of DNA flanking the xlnB locus of Streptomyces lividans
   reveals genes encoding acetyl xylan esterase and the RNA component of
   ribonuclease P.";
RN Gene 153:105-109(1995).
RP REVISION TO 225.
RA Sharack F.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Contributes to hydrolyze hemicellulose, the major
   component of plant cell-walls. XlnA and XlnB seem to act
   sequentially on the substrate to yield xylooligosaccharides and
   as carbon sources.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
   linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
   hydrolases).
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CC -----
DR EMBL, M64552; AAC06114.2; -.
DR HSSP, P09850; 1XNB.
DR InterPro, IPR001919; Bac_cellose-bind.
DR InterPro, IPR008965; Cellul bind.
DR InterPro, IPR008985; ConA like lec_g1.
DR InterPro, IPR001137; Glyco_hydro_11.
DR Pfam, PF00457; Glyco_hydro_11.1.
DR PRINTS, PR00911; GLHIDRLASE11.
DR SMART, SM00637; CBD_11.1.
DR PROSITE, PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE, PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation; Hydrolyase; Glycosidase; Signal.
FT CHAIN 1 41
FT SIGNAL 1 41
FT DOMAIN 42 230 ENDO-1,4-BETA-XYLANASE B.
FT DOMAIN 231 249 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 250 335 XYLAN-BINDING (POTENTIAL).
FT ACT_SITE 128 128 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 218 218 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 335 AA; 35575 MW; 513B1458B8F8FC0CF CRC64;
Query Match 55.5%; Score 585; DB 1, Length 335;
Best Local Similarity 54.0%; Pred. No. 2.8e-42; Indels 16; Gaps 5;
Matches 107; Conservative 34; Mismatches 41;

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DB 153 GTYDIYKTRVKNKDSVBGTRFPDQYWSVRQSKRTGCTTTTGNHPDAMARACMPLGNFSYX 212
QY 172 QIVAVEGYFSSGSASATV 189
DB 213 MIMAVEGYQSSGSSSINV 230
RESULT 11
ID XYNB CELFI STANDARD; PRT; 644 AA.
AC P54865;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Endo-1,4-Beta-xylanase D precursor (EC 3.2.1.8) (Xylanase D) (XYLD).
GN XYNB.
OS Cellulomonas fimi.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Cellulomonas.
OX NCBI_TaxID=1708;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=94224155; PubMed=8170339;
RA Millward-Sadler S.J., Poole D.N., Henriessat B., Hazlewood G.P.,
   Clarke J.H., Gilbert H.J.;
RT "Evidence for a general role for high-affinity non-catalytic
   cellulose binding domains in microbial plant cell wall hydrolases.";
RN Mol. Microbiol. 11:375-382(1994).
CC -!- FUNCTION: Endo-acting xylanase which displays no detectable
   activity against polysaccharides other than xylan. Hydrolyses
   glycosidic bonds with retention of anomeric configuration.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
   linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
   hydrolases).
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CC -----
DR EMBL, X76729; CA54145.1; -.
DR FIR, I40712; I40712.
DR PDB, 1ESB; 25-MAY-01.
DR PDB, 1ESB; 25-MAY-01.
DR PDB, 1HEH; 10-MAY-01.
DR PDB, 1HEH; 10-MAY-01.
DR PDB, 1XBD; 21-JUL-99.
DR PDB, 2XBD; 21-JUL-99.
DR InterPro, IPR001919; Bac_cellose-bind.
DR InterPro, IPR008965; Cellul bind.
DR InterPro, IPR008985; ConA like lec_g1.
DR InterPro, IPR001137; Glyco_hydro_11.
DR InterPro, IPR002509; Polysac_deacet.
DR Pfam, PF00457; Glyco_hydro_11.1.
DR Pfam, PF00457; Glyco_hydro_11.1.
DR Pfam, PF01522; Polysac_deacet; 1.
DR PRINTS, PR00911; GLHIDRLASE11.
DR SMART, SM00637; CBD_11.2.
DR PROSITE, PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE, PS00777; GLYCOSYL_HYDROL_F11_2; 1.
KM Xylan degradation; Hydrolyase; Glycosidase; Signal; Repeat;
   3D-structure.
FT CHAIN 1 43
FT SIGNAL 1 43
FT DOMAIN 44 64 ENDO-1,4-BETA-XYLANASE D.
FT DOMAIN 231 245 LINKER ("HINGE") (GLY-RICH BOX).
FT DOMAIN 246 644 2 X 88 AA APPROXIMATE CBD-LIKE REPEATS.

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FT REPEAT 246 333 1.
 FT REPEAT 557 644 2.
 FT DOMAIN 337 350 LINKER ("HINGE") (PRO-THR BOX).
 FT DOMAIN 548 556 LINKER ("HINGE") (GLY-RICH BOX).
 FT DOMAIN 231 238 POLY-GLY.
 FT DOMAIN 241 245 POLY-GLY.
 FT DOMAIN 548 558 POLY-GLY.
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 216 216 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 644 AA; 66581 MW; 56B045CC6E0E1820 CRC64;

Query Match 55.1%; Score 580.5; DB 1; Length 644;
 Best Local Similarity 56.2%; Pred. No. 1,4e-41;
 Matches 104; Conservative 37; Mismatches 39; Indels 5; Gaps 4;

QY 7 TGYHNGYFYSYWNDSHGVTMTLPGQGFVSVMNSGDFVGGKMGWPGTKNKVINFSGS 66
 Db TGTHDGYFYSFWTDSFGSVAMNDLNSGGGDT-RMSNTGNFVAGKMGWGTGR-KIVSYSGQF 106

QY 67 NPNKNSYLSYVGKSRNPLIEYIVENFGTNPSTGATKIGEVTCDSVYDIYRTQRYNA 126
 Db 107 NPNRNALTLTYGWTQSPLEIVYVDSWGYRPT-STFMGTVTSDGTYDIYRTQRYNA 164

QY 127 SIEG-STATFYQYVSVNRHRSQSVNTACHFNMAOHGLTGTMDYQIVAVEGYFSSGSA 185
 Db 165 SIEGSDSTFYQYVSVNRQKRTGTGTITSGNFDAMAKGMVLGRHNMIMATGEGYSSGSS 224

QY 186 SITVS 190
 Db 225 SITVS 229

RESULT 12
 XYNX_SCHCO STANDARD; PRT; 197 AA.

AC P35809; 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase A (EC 3.2.1.8) (Xylanase A) (1,4-beta-D-xylan
 DE xylanohydrolase A).
 GN XYNX.
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_Taxid=5334;

RP SEQUENCE
 RA STRAIN=ATCC 38548 / Delmar;
 RA Yaguchi M., Roy C., Ujile M., Watson D.C., Wakarchuk W.;
 RA (in) Visser J., Beldman G., Kusters-van Sommeren M.A.,
 RA Voragen A.G.J. (eds.);
 RL Xylans and xylanases, pp.149-154, Elsevier, Amsterdam (1992).
 RN [2]

RP SEQUENCE AND DISULFIDE BONDS.
 RC STRAIN=ATCC 38548 / Delmar;
 RC MEDLINE=94063044; PubMed=8243636;
 RA Ohts T., Roy C., Watson D.C., Wakarchuk W., Yaguchi M.,
 RA Jurassek L., Palce M.G.;
 RA "Amino acid sequence and thermostability of xylanase A from
 RT Schizophyllum commune";
 RT FEBS Lett. 334:296-300(1993).
 RN [3]

RP PARTIAL SEQUENCE, AND ACTIVE SITE GLU-87.
 RC STRAIN=ATCC 38548 / Delmar;
 RC MEDLINE=94155888; PubMed=7906649;
 RA Bray M.R., Clarke A.J.;
 RA "Identification of a glutamate residue at the active site of xylanase
 RT A from Schizophyllum commune";
 RT Eur. J. Biochem. 219:821-827(1994).
 CC -1- FUNCTION: Hydrolyzes xylans into xylobiose and xylose. This
 CC xylanase has a very broad pH activity.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic

CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
 DR PIR: A44597; A44597.
 DR HSPF: O43097; XYNX.
 DR InterPro: IPR008985; Consil-like_1ec_g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASB1.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase.
 FT ACT_SITE 87 87 NUCLEOPHILE (PROBABLE).
 FT ACT_SITE 184 184 PROTON DONOR (BY SIMILARITY).
 FT DISULFID 111 160
 SQ SEQUENCE 197 AA; 20978 MW; 42C8074E67C1FB59 CRC64;

Query Match 54.3%; Score 572.5; DB 1; Length 197;
 Best Local Similarity 55.0%; Pred. No. 1.7e-41;
 Matches 105; Conservative 35; Mismatches 44; Indels 7; Gaps 3;

QY 7 TGYHNGYFYSYWNDSHGVTMTLPGQGFVSVMNSGDFVGGKMGWPGTKNKVINFSGS 65
 Db 7 TGTDDGYFYSWMTDAGDATTQNNGGSYTLTMSGNNGNLVGGKMGWPGASRSISYSGT 66

QY 66 YNPNKNSYLSYVGKSRNPLIEYIVENFGTNPSTGATKIGEVTCDSVYDIYRTQRYNA 125
 Db 67 YQPNKNSYLSYVGKSRNPLIEYIVENFGTNPSTGATKIGEVTCDSVYDIYRTQRYNA 126

QY 126 PSIEGTAIFYQYVSVNRHRS-----SGSVNTACHFNMAOHGLTGT-MDYQIVAVEGY 179
 Db 127 PSIDGTOTFEDQFVSVNRKAPAGSGISGYDVQCHFPAMGLGNLGSNNHNYQIVAVEGY 186

QY 180 FSSGSGASITVS 190
 Db 187 QSSGTAITIVA 197

RESULT 13
 XYN2_MAGGR STANDARD; PRT; 233 AA.

AC P55335; Q01171; 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase 22 precursor (EC 3.2.1.8) (Xylanase 22)
 DE (1,4-beta-D-xylan xylanohydrolase 22).
 GN XYN2.
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; incertae sedis; Magnaporthaceae; Magnaporthe.
 OX NCBI_Taxid=148305;

RP SEQUENCE FROM N.A.
 RC STRAIN=KEN60-19;
 RC MEDLINE=96172742; PubMed=8589407;
 RA Wu S.C., Kaufman S., Darvill A.G., Albersheim P.;
 RA "Purification, cloning and characterization of two xylanases from
 RT Magnaporthe grisea, the rice blast fungus";
 RT Mol. Plant Microbe Interact. 8:506-514(1995).
 RL -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xyloisidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).

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 CC -----
 DR EMBL; L37529; AAC41683.1; -
 DR HSSP; O43097; 1XNB.
 DR InterPro; IPR008985; Consa_like lec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 39
 FT CHAIN 40 233
 FT ACT_SITE 126 126 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 217 217 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 233 AA; 25491 MW; 400963836F581F98 CRC64;
 Query Match 52.4%; Score 552.5; DB 1; Length 233;
 Best Local Similarity 50.8%; Pred. No. 1e-39;
 Matches 97; Conservative 34; Mismatches 57; Indels 3; Gaps 2;
 QY 1 OTIOPGTHNGVYFVSVMNDHGSGVTMTLGPQGFVSVMNSGDPFGKGMQPGTKNKYI 60
 Db 40 QSTPSSIGRHNGYIYSMTDASFPVQYQNGSGSISYQWOSGGSFVGKGMMPG-GSKSI 98
 QY 61 NFGSGSNP--NGNSYLSVYGSNRNPLIEYIVENFGTNPSTGATKLGVTCDGSYYDIY 118
 Db 99 TYSGTFPVNNNGNAYLCIYGMTQNPILVEYIILENRYGYNVNGNAGRGTLQAAGGYTLH 158
 QY 119 RTGRVNPSTIEGTATFYQVSVRRNRHSSGVSNTACHFNMAOHGLTGLTMDYQIVAVG 178
 Db 159 ESRVNVQPSLEGRTFOQYVAIRQQRKNSGTNTGTFPQAWERAGMGNMNTIVATG 218
 QY 179 YFSSGSASITV 189
 Db 219 YRSAGNSNINV 229
 RESULT 14
 XNXC STRLI STANDARD; PRT; 240 AA.
 AC P26250;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Endo-1,4-beta-xylanase C precursor (EC 3.2.1.8) (Xylanase C)
 DE (1,4-beta-D-xylan xylanhydrolase C).
 GN XNXC.
 OS Streptomyces lividans.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1916;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-80.
 RC STRAIN=66 / 1326;
 RX MEDLINE=92077439; Pubmed=1743521;
 RA Sharrock F., Roy C., Yaguchi M., Morosoli R., Kluepfel D.;
 RT "sequences of three genes specifying xylanases in Streptomyces
 lividans.";
 RL Gene 107:75-82(1991).
 CC -1- FUNCTION: Contributes to hydrolyze hemicellulose, the major
 CC component of plant cell-walls.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to cellulase family G (family 11 of glycosyl
 CC hydrolases).
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 CC -----
 DR EMBL; M64553; AAA26836.1; -
 DR EMBL; A25307; CAA01768.1; -
 DR PIR; JS0591; JS0591.
 DR HSSP; P09850; 1XNB.
 DR InterPro; IPR008985; Consa_like lec_g1.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR InterPro; IPR006311; Tac.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRASE11.
 DR TIGRFAMs; TIGR01409; TAT signal seq; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Xylan degradation; Hydrolase; Glycosidase; Signal.
 KM Xylan degradation; Hydrolase; Glycosidase; Signal.
 FT SIGNAL 1 49
 FT CHAIN 50 240
 FT ACT_SITE 134 134 NUCLEOPHILE (BY SIMILARITY).
 FT ACT_SITE 226 226 PROTON DONOR (BY SIMILARITY).
 SQ SEQUENCE 240 AA; 25673 MW; FC663415780142CA CRC64;
 Query Match 50.6%; Score 533; DB 1; Length 240;
 Best Local Similarity 53.6%; Pred. No. 4.6e-38;
 Matches 103; Conservative 31; Mismatches 48; Indels 10; Gaps 6;
 QY 2 TTOPGTHNGVYFVSVMNDHGSGVTMTLGPQGFVSVMNSGDPFGKGMQPGTKNKYIN 61
 Db 55 TNGQT---DGYISFTMDGGGSVMTLNGGGSISTGTGTCNFGYAGKMGSTGDN--VR 109
 QY 62 FSGSNPNNGSYLSVYGSNRNPLIEYIVENFGTNPSTGATKLGVTCDGSYYDIYQ 121
 Db 110 YNGYFNPNNGYGLCYGWTNPILVEYIIVDMWGSYRP-TGYTK-GTVSSDGFYDIYQTT 167
 QY 122 RVNAPSIEGTATFYQVSVRRNRHSSGVS--VNTACHFNMAOHGLTGLTMDYQIVAVG 178
 Db 168 RYNAPSVEGTATFYQVSVRRNRHSSGVSSTGTTGNHFDAMAPAGNNQGFYYIMATG 227
 QY 179 YFSSGSASITVS 190
 Db 228 YOSSGSNITVS 239
 RESULT 15
 XNNA BACST STANDARD; PRT; 210 AA.
 AC P45705;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase A precursor (EC 3.2.1.8) (Xylanase A)
 DE (1,4-beta-D-xylan xylanhydrolase A).
 GN XNNA.
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=No. 236;
 RA Cho S., Choi Y.;
 RT "Nucleotide sequence analysis of an endo-xylanase gene (xynA) from
 RT Bacillus stearothermophilus";
 RL J Microbiol. Biotechnol. 5:117-124(1995).
 CC [2]
 CC REVISIONS.
 CC STRAIN=No. 236;
 RA Cho S., Choi Y.;
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 30, 2004, 19:35:14 ; Search time 33 Seconds

(without alignments)
1816.620 Million cell updates/sec

Title: US-09-856-025B-65

Perfect score: 1054
Sequence: 1 QTIQPGTGHNGYFYSYMD.....YQIVAVEGYFSSGSASITVS 190

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPTRMBL_25:*
2: sp archaea:*
3: sp bacteria:*
4: sp fungi:*
5: sp human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvitus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	986	93.5	223	3	Q02244 trichoderma
2	974	92.4	223	3	Q09015 trichoderma
3	882	83.7	223	3	Q72803 trichoderma
4	858	81.4	220	3	Q8J0T4 trichoderma
5	829	78.7	223	3	Q9UVF9 trichoderma
6	739.5	70.2	241	3	Q12580 chaetomium
7	728.5	69.1	261	3	Q8J1V6 chaetomium
8	726.5	68.9	293	3	Q871E8 neurospora
9	678.5	64.4	219	3	Q12579 chaetomium
10	669.5	63.5	295	3	Q9C1R2 chaetomium
11	661.5	62.8	232	3	Q9HFA4 aspergillus
12	660.5	62.7	227	3	Q00263 ascomycota
13	656.5	62.3	290	3	Q9HE20 phanerochaete
14	656.5	62.3	290	3	Q9HE20 phanerochaete
15	654.5	62.1	227	3	Q9UV23 setosphaeria
16	643.5	61.1	346	2	Q8VUT4 pseudomonas

17	639.5	60.7	194	3	P81536 paecilomyces
18	638.5	60.6	230	3	Q8J1V5 chaetomium
19	633.5	60.1	225	3	Q8T222 aspergillus
20	632.5	60.0	338	2	Q56265 thermomonas
21	624.5	59.3	231	3	Q13447 cochlidiobolus
22	623.5	59.2	335	2	Q08346 streptomyces
23	623.5	59.2	335	2	Q9RMV4 streptomyces
24	621.5	59.0	335	2	Q9RQ88 promeliomonas
25	620	58.8	221	3	Q9U0Q2 penicillium
26	617.5	58.6	223	3	Q9HFH0 penicillium
27	617.5	58.6	231	3	Q00350 cochlidiobolus
28	603.5	57.3	344	2	Q8GMV7 nomomuraea
29	603	57.2	228	2	Q59962 streptomyces
30	601.5	57.1	231	3	Q72A57 gibberella
31	600.5	57.0	221	3	P87037 aspergillus
32	597.5	56.7	231	3	Q9C1R1 fusarium oxysporum
33	596.5	56.6	227	3	Q9HGE1 humicola grisea
34	594.5	56.4	329	2	Q9RMH9 streptomyces
35	591.5	56.1	283	3	Q96UV7 lentinula edodes
36	582	55.2	335	16	Q9RKN6 streptomyces
37	572	54.3	191	2	Q9EM89 streptomyces
38	572	54.3	216	3	Q74716 claviceps purpurea
39	536.5	50.9	241	16	Q9R172 streptomyces
40	534.5	50.7	361	2	Q52375 caldicelluligranulum
41	531	50.4	240	2	Q56013 streptomyces
42	524.5	49.8	656	2	Q59300 cellvibrrio
43	522.5	49.6	661	2	Q59674 pseudomonas
44	518	49.1	352	2	Q84DD2 pseudomonas
45	516.5	49.0	360	2	P77853 dictyoglomus

ALIGNMENTS

RESULT 1

Q02244 PRELIMINARY; PRT; 223 AA.

AC Q02244;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Endoxylanase II (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
GN XLN2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
OX NCBI_TaxID=51453;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94088442; PubMed=8264524;
RA Saarelainen R., Palohelmo M., Fagerstrom R., Suominen P.L.,
RA Nevalainen K.M.;
RT "Cloning, sequencing and enhanced expression of the Trichoderma reesei
RT endoxylanase II (PI 9) gene xln2.";
RL Mol. Genet. 241:497-503(1993).
CC -!- CATALYTIC ACTIVITY: ENDOPOLYMERIZATION OF 1,4-BETA-D-XYLOSIDIC
CC LINKAGES IN XYLANS.
CC -!- PATHWAY: XYLAN DEGRADATION.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILLY G (FAMILY 11 OF GLYCOSYL
CC HYDROLASES).
DR EMBL: S67387; AB29346.1; -.
DR PIR: S38883; S39883.
DR HSSP: P96217; IXIO.
DR GO: GO:0005453; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR008985; Cons. like lec_g1.
DR InterPro: IPR001137; Glyco_hydro_11.
DR Pfam: PR00457; Glyco_hydro_11; 1.
DR PRINTS: PR00911; GHYPRASE1.
DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
DR GlycoStase: Hydrolase; Xylan degradation.
KW SEQUENCE 223 AA; 24069 MW; 79668149EADA22F9 CRC64;

Query Match 93.5%; Score 986; DB 3; Length 223;
 Best Local Similarity 95.3%; Pred. No. 1,3e-69;
 Matches 181; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153
 QY 121 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180
 DB 154 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTAHFNAMAQHGTLTGMDYQIYAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 2

Q99015 PRELIMINARY; PRT; 223 AA.

AC Q99015; PRT; 223 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Beta-xylanase precursor (EC 3.2.1.8) (Bndo-1,4-beta-xylanase).
 OS Trichoderma reesei (Hypocrea jecorina).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Hypocreaaceae; Hypocrea.
 OX NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-QW 62;
 RX MEDLINE=97076932; PubMed=8975597;
 RA la Grange D.C., Pretorius I.S., van Zyl W.H.;
 RT "Expression of a Trichoderma reesei beta-xylanase gene (XYN2) in
 RT Saccharomyces cerevisiae";
 RL Appl. Environ. Microbiol. 62:1036-1044 (1996).
 CC -1- CATALYTIC ACTIVITY: ENDOPOLYSACCHARIDASE OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 DB EMBL; U24191; AAB50278.1; -.
 DB HSSP; P36217; 1XCO.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR006985; cona_like_rec_91.
 DR InterPro; IPR01137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLYHDRLASE11.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KM Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT SIGNAL
 FT CHAIN 1 223 POTENTIAL
 FT SEQUENCE 223 AA; 23981 MW; F696E545DAC90B84 CRC64;

Query Match 92.4%; Score 974; DB 3; Length 223;
 Best Local Similarity 94.2%; Pred. No. 1.1e-68;
 Matches 179; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120

DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153
 QY 121 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180
 DB 154 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTAHFNAMAQHGTLTGMDYQIYAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 3

Q728Q3 PRELIMINARY; PRT; 223 AA.

AC Q728Q3; PRT; 223 AA.
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase (EC 3.2.1.8).
 OS Trichoderma viride.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-YNUCC0183;
 RA Li W.P., Zhang Q., Liao C.L., Zhou J.G., Yang Y.H., Liu W.C.,
 RA Yang Z.W.;
 RT "Cloning and characterization of endo-1,4-beta-xylanase from
 RT Trichoderma viride YNUCC0183";
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY320048; AAP83925.1; -.
 KM Glycosidase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 223 AA; 24218 MW; F3APFBE76FA03CAE CRC64;

Query Match 83.7%; Score 882; DB 3; Length 223;
 Best Local Similarity 83.2%; Pred. No. 1.7e-61;
 Matches 158; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 60
 DB 34 QTIQPGTGHNGYFYSYWNDGSGVTMTLPGGQFSYVNSGDFVGGKGMQPGTKXKI 93
 QY 61 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 120
 DB 94 NFSGSYNPNNGSYLVYVWMSRNPLIEYIVENFGTNPSTGATKLGAVTCDGSVYDIYRT 153
 QY 121 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTACHFNAMAQHGTLTGMDYQIYAVEGYF 180
 DB 154 QRVNAPSIEGATFYQYWSYVRNRSSGSVNTAHFNAMAQHGTLTGMDYQIYAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 4

Q8J0T4 PRELIMINARY; PRT; 220 AA.

AC Q8J0T4; PRT; 220 AA.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Xylanase.
 OS Trichoderma sp. SY.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Trichoderma.
 OX NCBI_TaxID=215577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SY;
 RA Min S.Y., Kim B.G., Ahn J.-H.;
 RT "Purification, Characterization, and cDNA Cloning of Xylanase from

RT Fungus Trichoderma Strain SY.":
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY156910; AA078423.1; -.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; COA1_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR SEQUENCE 220 AA; 23814 MW; 10E8B7D5168B05EF CRC64;

Query Match 81.4%; Score 858; DB 3; Length 220;
 Best Local Similarity 81.1%; Pred. No. 1,3e-59;
 Matches 154; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 QTTPGTHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 60
 DB 31 QVIGPGTHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 90
 QY 61 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 120
 DB 91 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 150
 QY 121 QRYVAPSEGTATFYQWYSVRNRHRSQSVNTACHFNAAQHGTLTGMDYQIVAVEGYF 180
 DB 151 QRYVAPSEGTATFYQWYSVRNRHRSQSVNTACHFNAAQHGTLTGMDYQIVAVEGYF 210
 QY 181 SSGSASITVS 190
 DB 211 SSGSASITVS 220

RESULT 5
 Q9UVF9
 ID Q9UVF9; PRELIMINARY; PRT; 223 AA.
 AC Q9UVF9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8).
 OS Trichoderma viride.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; microsporitic Hypocreales; Trichoderma.
 CC NCBI_TaxID=5547;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Furman-Matarasso N., Cohen E., Avni A.;
 RT "Mutations in the Active Site of the Ethylene Inducing Xylanase
 RT Elicitor Inhibits the b-1-4-Endoxylanase Activity But Not the
 RT Elicitation Activity.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: A0102718; CAB60757.1; -.
 DR HSSP: P48793; 1XND.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; COA1_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR Glycosidase; Hydrolase; Signal; Xylan degradation.
 FT STGNL 1 33
 FT CHAIN 34 223
 FT CHAIN 223 223
 SEQUENCE 223 AA; 24230 MW; FB812028FB1212A CRC64;

Query Match 78.7%; Score 829; DB 3; Length 223;
 Best Local Similarity 78.4%; Pred. No. 2,5e-57;
 Matches 149; Conservative 14; Mismatches 27; Indels 0; Gaps 0;

QY 1 QTTPGTHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 60
 DB 34 QVIGPGTHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 93
 QY 61 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 120
 DB 94 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 153
 QY 121 QRYVAPSEGTATFYQWYSVRNRHRSQSVNTACHFNAAQHGTLTGMDYQIVAVEGYF 180
 DB 154 QRYVAPSEGTATFYQWYSVRNRHRSQSVNTACHFNAAQHGTLTGMDYQIVAVEGYF 213
 QY 181 SSGSASITVS 190
 DB 214 SSGSASITVS 223

RESULT 6
 Q12580
 ID Q12580; PRELIMINARY; PRT; 241 AA.
 AC Q12580;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Endo-beta-1,4-xylanase (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 OS Chaetomium gracile.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Sordariomycetidae; Sordariales; Chaetomiales; Chaetomium.
 CC NCBI_TaxID=47794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96118924; PubMed=8595661;
 RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;
 RT "Two family G xylanase genes from Chaetomium gracile and their
 RT expression in Aspergillus nidulans.";
 RL Curr. Genet. 29:73-80(1995).
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XILAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL: D49851; BAA08650.1; -.
 DR PIR: S71473; S71473.
 DR HSSP: P36217; 1XVO.
 DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR008985; COA1_1ec.g1.
 DR InterPro: IPR001137; Glyco_hydro_11.
 DR Pfam: PF00457; Glyco_hydro_11; 1.
 DR PRINTS: PR00911; GLHYDRASE11.
 DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR Glycosidase; Hydrolase; Xylan degradation.
 SEQUENCE 241 AA; 25564 MW; DCD4B012272777F CRC64;

Query Match 70.2%; Score 739.5; DB 3; Length 241;
 Best Local Similarity 71.6%; Pred. No. 2,8e-50;
 Matches 131; Conservative 22; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 66
 DB 38 TGYHNGYFYSYVNDGHGVTMTLGPQGQFSVWNSGDFVGKQKMGPTKRYI 96
 QY 67 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 126
 DB 97 NFGSYVNPNGSYLSVYGMGRNPLIEYIVENFGTYNPSTGATKLGVTCDGSDYDIYRT 156
 QY 127 SIEGTATFYQWYSVRNRHRSQSVNTACHFNAAQHGTLTGMDYQIVAVEGYF 186

DB 157 SIEGTSTFYQFWSVRNKRSGGSVNMAHFNMMAAQLGTHDYQIVATGEGYSSGSAT 216

QY 187 ITV 189

DB 217 VNV 219

RESULT 7

Q871E8 ID Q871E6 PRELIMINARY; PRT; 261 AA.

AC Q871E6;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endoxylanase 11A precursor.

GN XYN11A.

OS Chaetomium thermophilum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

OX NCBI_TaxID=209285;

RN [1]

RP SEQUENCE FROM N.A.

RA Mantyla A., Paloheimo M., Hakola S., Leskinen S., Vehmaopera J.,

RA Lantto R., Suominen P.;

RT "heterologous production of three xylanases from Chaetomium

RT thermophilum in Trichoderma reesei";

RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ508931; CAD48749.1; "

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR008985; ConA like lec gl.

DR InterPro; IPR001137; glyco hydro 11.

DR Pfam; PF00457; glyco hydro 11.

DR PRINTS; PR00911; GLHYDRLASE11.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

KM Signal; Xylan degradation; Hydrolyase; Glycosidase.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 261 ENDOXYLANASE 11A.

SQ SEQUENCE 261 AA; 27844 MW; 4206256334D7707 CRC64;

Query Match 69.1%; Score 728.5; DB 3; Length 261;

Best Local Similarity 66.8%; Pred. No. 2.2e-49;

Matches 127; Conservative 26; Mismatches 36; Indels 1; Gaps 1;

QY 1 QTI-QPGTGYHNGFYYSYNDGSHGVMTLPGPGQFVSVMNSGDFVVGKGMQPGTKNKV 59

DB 27 QTLLSSATGTHNGFYYSFWTDGQGNIRFNLESGQSVTMSGNMVGKGMPPGTDNEY 86

QY 60 INFGSYNPGNSYLSVYGNRNPLIEYIVENFGTYNPGTGATKLGVTTCDSYDTR 119

DB 87 INYADYRPNNGNSYLAVYGTWRNPLIEYVVESEFGYDPSGTATMGSVTTDGTYNIR 146

QY 120 TORVNASIEGTATFYQYWSVRNKRSGSVNTACHFNMAHQGLTIGTMDYQIVAVEGY 179

DB 147 TORVNASIEGTATFYQYWSVRNKRSGSVNTACHFNMAHQGLTIGTMDYQIVAVEGY 206

QY 180 FSSGSASITV 189

DB 207 YSSGSATVNV 216

RESULT 8

Q871E8 ID Q871E8 PRELIMINARY; PRT; 293 AA.

AC Q871E8;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Probable endo-1, 4-beta-xylanase B.

GN Neurospora crassa.

OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.

OX NCBI_TaxID=5141;

RN [1]

RP SEQUENCE FROM N.A.

RA Schulte U., Aign V., Hehseisel J., Brandt P., Fattmann B., Holland R.,

RA Nyakatura G., Mewes H.W., Mannhaupt G.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA German Neurospora genome project;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX294027; CAD71059.1; "

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004553; F:hydrolyase activity, hydrolyzing O-glycosyl . . .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR00254; CBD fungal.

DR InterPro; IPR008985; ConA like lec gl.

DR InterPro; IPR001137; glyco hydro 11.

DR Pfam; PF00734; CBM_1; 1.

DR Pfam; PF00457; glyco hydro 11.

DR PRINTS; PR00911; GLHYDRLASE11.

DR ProDom; PD01821; CBD fungal; 1.

DR SMART; SM00236; fcbd; 1.

DR PROSITE; PS00562; CBD FUNGAL; 1.

DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11.1; 1.

DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11.2; 1.

KM Glycosidase; Hydrolyase; Xylan degradation.

SQ SEQUENCE 293 AA; 30776 MW; D67A81CE65930F26 CRC64;

Query Match 68.9%; Score 726.5; DB 3; Length 293;

Best Local Similarity 69.4%; Pred. No. 3.6e-49;

Matches 127; Conservative 26; Mismatches 29; Indels 1; Gaps 1;

QY 7 TGYHNGFYYSYNDGSHGVMTLPGPGQFVSVMNSGDFVVGKGMQPGTKNKV 66

DB 42 TGTNGVYFYSFWTDGQGSVRYTNEAGQYATWSGNMVGKGMPPGT-DRTINVTGY 100

QY 67 NPNNGSYLSVYGNRNPLIEYIVENFGTYNPGTGATKLGVTTCDSYDTRVNP 126

DB 101 SPNNGSYLSVYGNRNPLIEYIVENFGTYNPGTGATKLGVTTCDSYDTRVNP 160

QY 127 SIEGTATFYQYWSVRNKRSGSVNTACHFNMAHQGLTIGTMDYQIVAVEGYSSGSAS 186

DB 161 SIDGTATFYQYWSVRNKRSGSVNTACHFNMAHQGLTIGTMDYQIVAVEGYSSGSST 220

QY 187 ITV 189

DB 221 INV 223

RESULT 9

Q12579 ID Q12579 PRELIMINARY; PRT; 219 AA.

AC Q12579;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Endo-beta1,4-xylanase A (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN CGXA.

OS Chaetomium gracile.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.

OX NCBI_TaxID=47794;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96118924; PubMed=8595661;

RA Yoshino S., Oishi M., Moriyama R., Kato M., Tsukagoshi N.;

RT "Two family G xylanase genes from Chaetomium gracile and their

RT expression in Aspergillus nidulans";

RL Curr. Genet. 29:73-80 (1995).

RL CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC

LINKAGES IN XYLANS.

-I- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

DR EMBL: D48850; BAA08649.1; -.

DR PIR: S71472; S71472.

DR HSSP: P36217; IXYO.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons. like lec.g1.

DR InterPro: IPR001137; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 219 AA; 23324 MW; 4729299E08DF9EBA CRC64;

Query Match 64.4%; Score 678.5; DB 3; Length 219;
Best Local Similarity 65.9%; Pred. No. 1.5e-45;
Matches 122; Conservative 25; Mismatches 37; Indels 1; Gaps 1;

QY 6 GTGHNAGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 65
GTGHNAGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 65

DB 36 GTGHNAGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 94
GTGHNAGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 94

QY 66 YNPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 125
YNPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 125

DB 95 FSPGNGYLAIVGWTQNPVEYIVESFGTYDPSQSKFGTQQDDSTYTTAKTRVNO 154
FSPGNGYLAIVGWTQNPVEYIVESFGTYDPSQSKFGTQQDDSTYTTAKTRVNO 154

QY 126 PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 185
PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 185

DB 155 PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 214
PSIRGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 214

QY 186 SITVS 190
SITVS 190

DB 215 SITVS 219
SITVS 219

RESULT 10

Q9C1R2 PRELIMINARY; PRT; 295 AA.

AC Q9C1R2; 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Xylanase 5 protein (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XYL5.

OS Fusarium oxysporum f. sp. lycopersici.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.

NCBI_TaxID=59765;

[1]

RP SEQUENCE FROM N.A.

RA Herra C., Gomez-Gomez E., Roncero M.; "Cloning and characterization of two family 11 xylanase genes in Fusarium oxysporum f. sp. lycopersici."

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

DR EMBL: AF246830; AAK2974.1; -.

DR HSSP: O43097; IYNA.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons. like lec.g1.

DR InterPro: IPR001137; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRASE11.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 295 AA; 30858 MW; CA41056DCD3C104 CRC64;

Query Match 63.5%; Score 669.5; DB 3; Length 295;
Best Local Similarity 63.6%; Pred. No. 1.1e-44;
Matches 117; Conservative 28; Mismatches 38; Indels 1; Gaps 1;

QY 7 TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 66
TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 66

DB 40 SCTNNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 98
SCTNNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 98

QY 67 NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126
NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126

DB 99 KPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 158
KPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 158

QY 127 SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 186
SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 186

DB 159 SIDGTQYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 218
SIDGTQYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 218

QY 187 ITVS 190
ITVS 190

DB 219 ITVS 222
ITVS 222

RESULT 11

Q9HFA4 PRELIMINARY; PRT; 232 AA.

AC Q9HFA4; 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Xylanase G2 (EC 3.2.1.8) (Endo-1,4-beta-xylanase).

GN XYG2.

OS Aspergillus oryzae.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

NCBI_TaxID=5062;

[1]

RP SEQUENCE FROM N.A.

RA Kimura T., Sakka K., Ohmura K.; "Molecular cloning, overexpression, and purification of major xylanase from Aspergillus oryzae."

RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RL -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-XYLOSIDIC LINKAGES IN XYLANS.

CC -1- PATHWAY: XILAN DEGRADATION.

CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY G (FAMILY 11 OF GLYCOSYL HYDROLASES).

DR EMBL: AB044941; BAB20794.1; -.

DR PIR: JC7577; JC7577.

DR HSSP: P36217; IXYO.

DR GO: GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . IEA.

DR GO: GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro: IPR008985; Cons. like lec.g1.

DR InterPro: IPR001137; Glyco_hydro_11.

DR Pfam: PF00457; Glyco_hydro_11; 1.

DR PRINTS: PR00911; GLHYDRASE11.

DR PROSITE: PS00776; GLYCOSYL_HYDROL_F11_1; 1.

DR PROSITE: PS00777; GLYCOSYL_HYDROL_F11_2; 1.

KW Glycosidase; Hydrolase; Xylan degradation.

SEQUENCE 232 AA; 24605 MW; 1F73104751EA561C CRC64;

Query Match 62.8%; Score 661.5; DB 3; Length 232;
Best Local Similarity 64.5%; Pred. No. 3.4e-44;
Matches 118; Conservative 28; Mismatches 36; Indels 1; Gaps 1;

QY 7 TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 66
TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 66

DB 50 TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 108
TGNHNGYFYSYVNDGAGVTMTLGPQGQFVSVMNSGDFVGGKMGQPTKRVINPSSG 108

QY 67 NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126
NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 126

DB 109 NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 168
NPNNGSYLVYGSNRPLEIYIVENFGTNPSTGATKLGVTCCGSYYDIYRTQRYNA 168

QY 127 SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 186
SIEGATFYQYVSVNRNHRSSGSVNTACHFNMAOCHGLTGMDOYIVAVEGYFSSGSA 186

Db 169 SIIGTATFTQFWSVRSKRVGIVTGTGNNFNMAKYGTLTGTHNYQIVATEGYQSSGSSA 228
 Qy 187 ITV 189
 Db 229 ITV 231

RESULT 12
 Q00263 PRELIMINARY; PRT; 227 AA.
 AC Q00263;
 DT 01-NOV-1986 (Tremblrel. 01, Created)
 DT 01-NOV-1986 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Endo-1,4-beta-xylanase precursor (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 OS Ascochyta pisi.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 CC Mitosporic Pezizomycotina; Ascochyta.
 CC NCBI_TaxID=47971;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lubbeck P.S., Paulin L., Degert Y., Lubbeck M., Collinge D.;
 RT "Molecular cloning and DNA sequencing of a xylanase gene from the
 RT phytopathogenic fungus Ascochyta pisi lib.;"
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASES OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; Z68891; CA93120.1; -;
 DR HSSP; 043097; IYNA
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR008985; Cons_Like_Lec_51.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 DR GlycoSIDase; Hydrolase; Signal; Xylan degradation.
 KW SIGNAL 1
 FT SIGNAL 19 POTENTIAL.
 SQ SEQUENCE 227 AA; 24010 MW; 692AE1FAE035CF0F CRC64;

Query Match 62.7%; Score 660.5; DB 3; Length 227;
 Best Local Similarity 63.7%; Pred. No. 4e-44;
 Matches 123; Conservative 21; Mismatches 44; Indels 5; Gaps 2;

Qy 2 TIGPGT---GYHNGFYSYMNDGSGVTMTLGPQGQFVSVMNSGDPFGKGMQPGTKN 57
 Db 34 TARAGTPSSQGTNHCFCYSWMTDGAQATYTNAGAGSISVNMKTGMLVGKGMNFGAA- 92
 Qy 58 KVINFGSGYNPNNGSYLSYVGWMSNPLIEYIYVENFETNPSTGATLGEVTCDSGVYDI 117
 Db 93 RTITVSGTYSFSGSYLAVGWTNPLIEYIYVENFETNPSTGATLGEVTCDSGVYDI 152
 Qy 118 YRTORVAPSIETGATFYQYWSVRRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 177
 Db 153 AQTQRTNQPISDGTQFQYQWSVRQNRSSGSVNMKTHFPAWAKMKGTGTHNYQIVAVE 212
 Qy 178 GYFSSGSASITVS 190
 Db 213 GYFSSGSASITVN 225

RESULT 13
 Q09HEZ0 PRELIMINARY; PRT; 290 AA.
 AC Q09HEZ0;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 OS Phanerochaete chrysosporium.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Aphyllophorales; Corticiaceae; Phanerochaete.
 CC NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Khan S.N., Loefer-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASES OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301904; AAG44994.1; -;
 DR HSSP; P00725; 1A26.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; Cons_Like_Lec_51.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; CBM_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fCBD; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW GlycoSIDase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 GN XYNB.
 OS Phanerochaete chrysosporium.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Aphyllophorales; Corticiaceae; Phanerochaete.
 CC NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;
 RA Khan S.N., Loefer-Corral O., Aspinall T.V., Sims P.F.G.;
 RT "Molecular characterization and expression analysis of two endo-1,4-B-
 RT xylanase genes from Phanerochaete chrysosporium."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOMETHYLASES OF 1,4-BETA-D-XYLANSIDIC
 CC LINKAGES IN XYLANS.
 CC -1- PATHWAY: XYLAN DEGRADATION.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY G (FAMILY 11 OF GLYCOSYL
 CC HYDROLASES).
 CC EMBL; AF301904; AAG44994.1; -;
 DR HSSP; P00725; 1A26.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR000254; CBD_fungal.
 DR InterPro; IPR008985; Cons_Like_Lec_51.
 DR InterPro; IPR001137; Glyco_hydro_11.
 DR Pfam; PF00457; CBM_1; 1.
 DR Pfam; PF00457; Glyco_hydro_11; 1.
 DR PRINTS; PR00911; GLHYDRLASE11.
 DR ProDom; PD001821; CBD_fungal; 1.
 DR SMART; SM00236; fCBD; 1.
 DR PROSITE; PS00776; GLYCOSYL_HYDROL_F11_1; 1.
 DR PROSITE; PS00777; GLYCOSYL_HYDROL_F11_2; 1.
 KW GlycoSIDase; Hydrolase; Xylan degradation.
 SQ SEQUENCE 290 AA; 30425 MW; 6D1C6415370A667D CRC64;

Query Match 62.3%; Score 656.5; DB 3; Length 290;
 Best Local Similarity 61.6%; Pred. No. 1.1e-43;
 Matches 117; Conservative 28; Mismatches 44; Indels 1; Gaps 1;

Qy 1 QTIQPGTGNHNGFYFSYVNDGSGVTMTLGPQGQFVSVMNSGDPFGKGMQPGTKN 60
 Db 34 QTPAGTPTNNNGFYFSYVNDGSGVTMTLGPQGQFVSVMNSGDPFGKGMQPGTKN 92
 Qy 61 NFSGSYNPNNGSYLSYVGWMSNPLIEYIYVENFETNPSTGATLGEVTCDSGVYDI 120
 Db 93 SFTANYQGNNGSYLSYVGWMSNPLIEYIYVENFETNPSTGATLGEVTCDSGVYDI 152
 Qy 121 ORVNAPSIETGATFYQYWSVRRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 180
 Db 153 TRVNEPSTIGTATFYQYWSVRRNRSSGSVNTACHFNMAQHGTLTGMDYQIVAVE 212
 Qy 181 SSGSASITVS 190
 Db 213 SSGSSTIVN 222

RESULT 14
 Q09HEY9 PRELIMINARY; PRT; 290 AA.
 AC Q09HEY9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Endo-1,4-B-xylanase B (EC 3.2.1.8) (Endo-1,4-beta-xylanase).
 OS Phanerochaete chrysosporium.
 CC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 CC Aphyllophorales; Corticiaceae; Phanerochaete.
 CC NCBI_TaxID=5306;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ME446;

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ORGANISM: Trichoderma harzianum
 STRAIN: Trichoderma harzianum, 20KD
 IMMEDIATE SOURCE:
 POSITION IN GENOME:
 FEATURE:
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi M., Roy C., Watson D.C., Rollin
 AUTHORS: F. Tan L.U.L., Senior D.J., & Saddler
 AUTHORS: J.N.
 TITLE:
 JOURNAL: Xylans and Xylanases
 VOLUME:
 ISSUE:
 PAGES: 435-438
 DATE: 1992
 DOCUMENT NUMBER:
 FILING DATE:
 PUBLICATION DATE:
 RELEVANT RESIDUES IN SEQ ID NO:
 US-08-044-621D-28

Query Match 95.3%; Score 996; DB 1; Length 190;
 Best Local Similarity 94.7%; Pred. No. 4,4e-85;
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSSYNDHGGVYTYNPGGQSFVYNSNSGNFVGKGMQPGTKXKVI 60
 DB 1 QTIQGTGYSNGYYSYNDHGGVYTYNPGGQSFVYNSNSGNFVGKGMQPGTKXKVI 60
 QY 61 NFSGSYNPNSYSLTYGMSRNPLEYIYVENFGTYNPGTATLGEVTSDSGVYDIYRT 120
 DB 61 NFSGSYNPNSYSLTYGMSRNPLEYIYVENFGTYNPGTATLGEVTSDSGVYDIYRT 120
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAQOGLTLGTMQYQIVAVEGYF 180
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAQOGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 12
 US-08-709-912-14
 Sequence 14, Application US/08709912
 Patent No. 5759840

GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wang L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
 STREET: 277 Park Ave.
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10172-0194
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,912
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Olsen Mr, Warren E
 REGISTRATION NUMBER: 27290

REFERENCE/DOCKET NUMBER: 1039.2000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-2400
 TELEFAX: (212) 758-2982
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 190 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 ORIGINAL SOURCE:
 ORGANISM: Trichoderma harzianum
 PUBLICATION INFORMATION:
 AUTHORS: Yaguchi, M
 AUTHORS: Roy, C
 AUTHORS: Watson, D. C.
 AUTHORS: Rollin, F
 AUTHORS: Tan, L. U. L.
 AUTHORS: Senior, D. J.
 AUTHORS: Saddler, J. N.
 JOURNAL: Xylan and Xylanase
 PAGES: 435-438
 DATE: 1992
 US-08-709-912-14

Query Match 95.3%; Score 996; DB 1; Length 190;
 Best Local Similarity 94.7%; Pred. No. 4,4e-85;
 Matches 180; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 QTIQPGTGYNNNGYFYSSYNDHGGVYTYNPGGQSFVYNSNSGNFVGKGMQPGTKXKVI 60
 DB 1 QTIQGTGYSNGYYSYNDHGGVYTYNPGGQSFVYNSNSGNFVGKGMQPGTKXKVI 60
 QY 61 NFSGSYNPNSYSLTYGMSRNPLEYIYVENFGTYNPGTATLGEVTSDSGVYDIYRT 120
 DB 61 NFSGSYNPNSYSLTYGMSRNPLEYIYVENFGTYNPGTATLGEVTSDSGVYDIYRT 120
 QY 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAQOGLTLGTMQYQIVAVEGYF 180
 DB 121 QRVNQPSTIGTATFYQYWSVRNRHSSGSVNTANHFNMAQOGLTLGTMQYQIVAVEGYF 180
 QY 181 SSGSASITVS 190
 DB 181 SSGSASITVS 190

RESULT 13
 US-09-047-370-14
 Sequence 14, Application US/09047370
 Patent No. 5866408

GENERAL INFORMATION:
 APPLICANT: Sung Dr., Wang L
 APPLICANT: Yaguchi Dr., Makoto
 APPLICANT: Ishikawa Dr., Kazuhiko
 TITLE OF INVENTION: Modification of Xylanase to Improve
 TITLE OF INVENTION: Thermophilicity, Alkalophilicity and
 TITLE OF INVENTION: Thermostability
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitzpatrick, Cella, Harper, and Scinto
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 CITY: New York
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 COUNTRY: USA
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 OPERATING SYSTEM: PC-DOS/MS-DOS

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